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U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

SEARCH REQUEST FORM

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Requestor's		Serial		
Name:		Number:		
Date:	Phone:		Art Unit:	
Search Topic: Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).				
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STAFF USE ONLY				
Date completed: 05-01-03 Searcher: Beverly 640	Search		Vendors	IG Suite
Terminal time: 20		CM-1		STN
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Total time: 23		N.A. Sequenc		Geninfo
Number of Searches:	:	A.A. Sequenc	e	SDC DARC/Questel
Number of Databases:		StructureBibliographic		Other CGN

PTO-1590 (9-90) + U.S. GPO: 1995-398-798/22489 USCOMM-DC 90-3952

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GenCore version 5.1.4_-p5_-4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a

em_htgo_other:*

AFUYBU31 11-SEP-2000 HOMO sapiens acyl Co-A: cholesterol acyltransferase-2 (ACAT2) mRNA, complete cds.

LOCUS DEFINITION

RESULT 1 AF099031 ACCESSION

AF099031.2 GI:4878036

Homo sapiens. Homo sapiens

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

ALIGNMENTS

502510

F331502S13

Sequence

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 1569)

Chang, C.C., Sakashita, N., Ornvold, K., Lee, O., Chang, E.T., Dong, R., Lin, S., Lee, C.Y., Strom, S.C., Kashyap, R., Fung, J.J., Farese, R.V.

AB075946 Rattus no BC025931 Mus muscu AF078751 Mus muscu S81092 acyl-coenzy L42293 Mus musculu D86373 Rattus norv AF053336 Chloroceb L21934 Homo saplen BC028940 Homo sapi AR053912 Sequence AR080271 Sequence II7130 Sequence 3 AF053337 Macaca fa AF354623 Pongo pyg AR083311 Sequence AR080270 Sequence 117129 Sequence 2 AF331507 Homo sapi AF332858 Homo sapi Continuation (4 of AC073573 Homo sapi AC068888 Homo sapi U65393 Oryctolagus AC110347 Rattus no Homo sapi Homo sapi AF099031 Homo sapi AF059203 Homo sapi U47320 Cricetulus AF354622 Gorilla g Drosophil Drosophil AC123791 Mus muscu AF331515 Homo sapi AC024216 Homo sapi Drosoph1. Drosophi Drosophi score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES F331502S06 AF332857S2 MUSACACT D86373 AF099031 AF059203 \$81092 10 DB 11:1 163811 11:0 174310 11:0 186322 11:0 242566 10:9 2102 10:8 156297 9:6 176 Length 919 157807 19371 Query Match 405.6 Score 34 33 33 33 33 33 33 Result

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/protein_id="aAAG398.1"
/db_xref="agyl 3746535"
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Oelkers,P., Cromley,D., Behari,A., Billheimer,J.T. and Sturley,S.I Direct Submission
Submitted (13-APR-1998) Human Nutrition, Columbia University, 630
W. 168th Street, New York, NY 10032, USA
Location/Qualifiers
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Oelkers, P., Behari, A., Cromley, D., Billheimer, J.T. and Sturley, S.I. Characterization of two human genes encoding acyl coenzyme A:cholesterol acyltransferase-related enzymes J. Biol. Chem. 273 (41), 26765-26771 (1998)
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Cercopithecus.
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Identification of a form of acyl-CoA:cholesterol acyltransferase specific to liver and intestine in nonhuman primates
J. Biol. Chem. 273 (41), 26747-26754 (1998)
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Boulevard, Winston-Salem,
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/organism="Cercopithecus aethiops"
/db_xref="taxon:9534"
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School of Medicine, Medical Center
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Direct Submission
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/product="acyl-CoA:cholesterol acyltransferase 2"
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NY STWMVYVHBWLYSYVYQDGLWLLGAQARGVAMLGVFLVSANHETFF
PVMILIELIVIGGMARFWHDQHTGPAWNVLMWTMLFLGGGIQVSLYCQEWYARRHCPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       589 ACGGGCCTGGGCTGTGCGCCTTTTAGCCGCCCACGCCGTGGTGCTCTGCGCGCTGCTGCGGTC
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                                                                                                                                                                                                                                                                    Length 2078;
                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                     Score 1459; DB 9;
Pred. No. 9.9e-282;
                                                                                                                                                                                                                                                                                                         0; Mismatches
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/db_xref="GI:219392929"
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                                                                                   Japan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 ACTGAGACGCACAGAGCCCCGGACTTGGTACAATGGACCCGACACATGGAGGCTGTGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGCTATACAATCCTACCCATCACAAGACAAACCTCTGCCCCCCACCTCCCCCAGGTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       268 TTGAGCAGGACCCAGGAGCCATCCCTGGGGAAACAGAAAGTTTTCATCATCCGCAAGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGCTGGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           508 TGGGTGCCCATGTTTCTGTCCACCCTGTTGGCGCCCGTACCAGGCCCTACGGCTGTGGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 1933;
                                Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

Furuichi (Bio.mie-u.ac.jp, Tel:81-59-231-9612, Location/Qualifiers
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                                                                                                                                                                                        /organism="Rattus norvegicus"
/db_xref="taxon:10116"
2 (bases 1 to 1933)
Yukio,F., Katsunori,M. and Takeshi,O.
Direct Submission
Submitted (11-DEC-2001) Furuichi Yuki
Bioresources; Kamihama, Tsu, Mie pref
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Pred. No. 7.86
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Best Local Similarity 83.5%;
Matches 1298; Conservative
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transferase 2,
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Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus mRNA for AcylCoA:Cholesterol Acyltransferase complete cds. AB075946.1 GI:21392391
                                                                                                                                                                                                                                                                                                                                                                                                    1128
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                                                                                                                                                                                                                                    CGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGTGCCCTG 1008
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                                                                                                                                                                                                                                                                                                               TTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCAACTACCGCACTTGGAACGTG
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                                                                                                                                                GTGGCCAAGAACTTTGCCCAGGCCCTGGGATGTGTGTGCTCTATGCCTGCTTCATCCTGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Katsunori,M., Takeshi,O. and Yukio,F.
Cloning and sequence of rat intestinal ACAT2
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; (Rodentia;
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Rattus norvegicus
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Mammalia; Eutheria;
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AB075946
LOCUS
DEFINITION
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/product="Similar to sterol o-acyltransferase 2"
/product="Gamanaspar.1."
/db_xref="Ga:1684142"
/translation="MOPKVPQLRRREGLGEEQEKGARGGEGNARTHGTPDLVQWTRHM
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QLPLALMTWVPMFLSTLLVPYQTLWLWARPRAGGAWMLGASIGCVLLAAHAVVLCVLP
PHYSVHELEPPASRCVLVFEOVRLLMSSFFLRETYPOIFCVRGGKGTSPPSFSSYLY
FLCPPLIYERTYPRETYPOIFCVRGMAGGASTLL
FLCPPLIYERTYPETREPSIRANYVARNEAOVLGCLLLAGALCVPVFANNSREPF
STRALLLSILHATGFGIFMLLLIFFAPLHCWLNAFAEMLRFGDRMFYRDWNNSTFFN
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VMLMLFLVFGGLLNFTMNDRHTGPAMNILMWTFLFMGQGIQVSLYCQEWYARRHCPLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Eltitida Heisao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Danes Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 57 Row: f Column: 19 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6755597. Location/Qualifiers
                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2170)
                                                                                                                                                      Submitted (18-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGCAGAGGACAGAAGGGCTGGGAGGGGAGCGGGAGCGCCAACCCTGT---GGAGATGGA
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                                                                                                                                                                                                                                                                                     Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
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Pred. No. 6.5e-213;
0; Mismatches 245;
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/tissue_type="Liver, normal. 5 m
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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83.3%;
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Best Local Similarity 83.3'
Matches 1297; Conservative
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                                                                                                                                              Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                info@bcgsc.bc.ca
                                                                                                                     Strausberg, R.
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                            TACCCTAGGACGCCCTATGTCAGGTGGAATTATGTGGCCCAGGAACTTTGCCCCAGGCCCTG
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DEFINITION

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VERSION KEYWORDS

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                                                                                TCCTTGAGCAGGACCCAGGAGCCATCCCTGGGGAAACAGAAGTTTTCATCATCCGCAAG 324
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          TCCCTGCTTGATGAGCTGATGGAGGTGCAGCATTTCCGCACCATCTACCACATGTTCATC
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AAGGCACAATTGCTGGAGCAAGCGCAGGGACAACTGAGGGAGCTGCTGGATCGGGCCATG
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                                        CGGGAGGCTATACAATCCTACCCATCACAAGACAAACCTCTGCCCCCACCTCCCCCAGGT
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AF078751 1607 bp mRNA linear ROD 15-OCT-1998 Mus musculus acyl coenzyme A:cholesterol acyltransferase-2 (Acact-2) mRNA, complete cds.
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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi

Bukaryota: Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus

(bases 1 to 1607)

(bases, S., Novak, S., Zheng, Y.W., Myers, H.M., Lear, S.R., Sande, E., Welch, C.B., Lusis, A.J., Spencer, T.A., Krause, B.R., Erickson, S.K.

and Farese, R.V. Jr.

ACAT-2, a second mammalian acyl-CoA:cholesterol acyltransferase.

Its cloning, expression, and characterization

J. Biol. Chem. 273 (41), 26755-26764 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/strain="C57BL/6"
/db_xref="taxon:10090"
/chromosome="15"
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Farese, R.V. Jr.
Direct Submission
Submitted (16-JUL-1998) Gladstr
Francisco, CA 94110, USA
Location/Qualifiers
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30. .1607
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Matches 1295; Conservative
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entry [NCBI gibbsq 175976] from the original journal article.
This sequence comes from Fig. 3A.
Location/Qualifiers
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                                                                                 1393 CATGACCAGCGCACCGGCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGC
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Tissue-specific expression and cholesterol regulation of acylcoenzyme A:cholesterol acyltransferase (ACAT) in mice. Molecular cloning of mouse ACAT cDNA, chromosomal localization, and regulation of ACAT in vivo and in vitro J. Biol. Chem. 270 (44), 26192-26201 (1995)
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1176 AGGAGCCCTTCAGTGCTCGTGTCCTGGTCTGTGTGTTTAACTCCATCTTGCCAGGTG 1235
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Mus musculus CDNA to mRNA.
Mus musculus cDNA to mRNA.
Bukarnyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
(bases 1 to 3697)
Uelmen, P.J., Oka,K., Sullivan,M., Chang,C.C., Chang,T.Y. and
                                                                            1476 CCCTGTCGCCTGTGGTGCACGAGTATGCCCTCGCCATCTGCCTGAGTTACTTCTACCCCG
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                                                 TCTTCATGCTGCTCATCTTCTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCCG
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ROD 21-NOV-1995

1462

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus

1162 2019

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Matsuda, H., Hakamata, H., Kawasaki, T., Sakashita, N., Miyazaki, A., Takahashi, K., Shichiri, M. and Horiuchi, S. Molecular cloning, functional expression and tissue distribution of rat acyl-coenzyme A:cholesterol acyltransferase Biochim. Biophys. Acta 1391 (2), 193-203 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus mRNA for acyl-coenzyme A:cholesterol acyltransferase, complete cds.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
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                                          1043 TCTTCATGCTGCTGCTCATCTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCCG 1102
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                   GGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGTG
                                                                                                 TGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCC
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Direct Submission
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RARABELKPEWEWGCHFPDFVTNLIEKSASLDNGGCALTFFSILEBWKNHHRANDL
RAPPEQGKIFISNGSLDELFEVDHIRTIYHMFIALLILFVLSTIVVDYIDEGRLVLE
FNLLAYAFGKFPTVIWTWMANFLSTLSIPYFLFQPWAHGYSKSSHPLIYSLVHGLLFL
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SKDPLPTVNQYLYFLFAPTLIYRDNYPRTPTVRWGYVAMQFLQVFGCLFYVYYIFERL
CAPLFRNIKQEPFSARVLVLCVFNSILPGVLILFLSFFRFLHCWLNAFAEMLRFGDRM
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EYALAICLSYFYPVLFVLFWFFGMAFNFIVNDSRKRPIWNIMVWASLFLGYGLILCFY
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/product="acyl-coenzyme A: cholesterol acyltransferase"
/protein_id="AAC42075.1"
/brotein_id="1066810"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 CATCCCTGGGGAAACAGAAAGTTTTCATCCTCCCAAGTCCCTGCTTGATGAGCTGATGG 346
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                                                                                                                                                            amino acid feature: N-glycosylation site, aa 481"
                                                                                                                                         /note="amino acid feature: N-glycosylation site,
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59.2%; Pred. No. 3.5e-74;
Live 0; Mismatches 506;
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753. .760
/gene="ACACT"
761. .>1016
/gene="ACACT"
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3697
                                                                                                                /gene="ACACT"
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/db_xref="G1:3036905"
/tb_xref="G1:3036905"
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RAKDLRAPPEQGKIFISRRSLLDELFFEVDHIRTIYHMFIALLIIFILSTLVVDYIDEG
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ARFETVROLGIGGFPYVLAYTLPPASRFLILIGOTRLWYKAHSYVEKBVPRVLSA
ARFETVROLGIGGFPTVVLAYTLPPASRFLILIGOTRLWYKAHSYVEKBVPRVLSA
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IFERLCAPLFRNIKQEPFSARVLVLCVFNSILDFGVLMLFLSFFAFLHCMLNAFAEMLR
FGDRHYKWMNSTSYSNYYEWNVVHDWLYYYYKKDLLWFFSKRFRFAAMLAVFAL
SADVHBYALAYCLSYFYPVLFYLEMFFGMAFRFIVNDSRKRFWWNIMVRASLFLGHGV
ILCFYSGEWTARQFCFLKNFFTEMFFGMAFRFIVNDSRKRFWWNIMVRASLFLGHGV
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      Kumamoto University School
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Location/Qualifiers
                                                                                                                                                                                                     A:cholesterol acyltransferase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 412.2; DB 10; Length 1750;
Pred. No. 2.6e-72;
0; Mismatches 513; Indels 24;
                                                                                            /organism="Rattus norvegicus"
                                                                                                                                                     /tissue_type="adrenal grand"
92. .1729
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/product="acyl-coenzyme
                                                                                                                        /db_xref="taxon:10116"
/sex="male"
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                                                                                                         /strain="Wistar"
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ilarity 58.7%;
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AF053336 16-1999 acyl-CoA:cholesterol acyltransferase 1 (ACAT1)
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Gercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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                    1197 TGCTGATGCTGTTCCTTTGCTTTTTGCACTGCTGCTCAATGCCTTTGCTG
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GGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGTG
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                                                                          TGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTTTTGCCAACATGAGCC
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YLDGRALVELESELLSYRAGKFPTVWWWIMELSTFSVPYFLPGRWATGYSKSSHPLI
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LGNGYLLCFYSQEWYARQHEVLEWFFSKAPTVNVHDSKKKPIWNVMMTSLF
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Direct Submission
Submitted (11-MAR-1998) Internal Medicine, Wake Forest University
School of Medicine, Medical Center Boulevard, Winston- Salem, NC
27157, USA
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                                                                                                                                                                              /EC_number="2.3.1.26"
/function="catalyzes formation of fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                aethiops"
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/organism="Cercopithecus aethiops"
/db_xref="taxon:9534"
---"^Archal"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 410.4; DB 9;
Pred. No. 6e-72;
0; Mismatches 506;
                                                                                                                  /note="synonym: Cercopithecus
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                                                                                                      /tissue_type="adrenal"
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Homo sapiens acyl-coenzyme A: cholesterol acyltransferase mRNA,
complete cds.
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1 (bases 1 to 4011)

Chang, C.C., Huh, H.Y., Cadigan, K.M. and Chang, T.Y.

Molecular cloning and functional expression of human acyl-coenzyme A:cholesterol acyltransferase cDNA in mutant Chinese hamster ovars
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                         GIGCICIAIGCCIGCITCAICCIGGGCCCCTCIGIGITCCIGICITIGCCAACAIGAGC
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G-----CTACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCT
                                                                                          AGGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGT
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                                                                                                                                                                                                                                      CAGGAGCCCTTCAGCGCTCGTGTTCTGGTCCTATGTGTATTTAACTCCATCTTGCCAGGT
                                                                       2217 ACGTGCCTCGGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCAATACCTACA
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                                           CTGTGCCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGGATCCAGGCCCCCAGTTTCTCCA
                                                                                                     G-----CTACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCT
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FYYYYTERLCAPLEFNIYOROPFSARVOYLOVFNSTILPGULILFLTFFAFLHCWLNAF
AEMLARGDRMEYKDWNSTSYSOYYYTEWNYVYHDWLYYYAYKDFLURFSKRRYSAAMI
AVFAVSAVVHEYALAVCLSFFYPVLFVLFWFFGMAFNFIVNDSRKKPIWNVLMWTSLF
1384 . 3389
3962 . 3967
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KQLIAKKIKLTAEAEELKPFFWKEVGSHFDDFVTNLIEKSASLDNGGCALTTFSVLEG
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YIDEGRLVLEFSLLSYAFGKFPTVVWTWMIMFLSTFSVPYFLFOHWATGYSKSSHPLI
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/protein_id="AAC37532.2"
/db_xref="GI:4878022"
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Chang,C.C. and Chang,T.Y.
Direct Submission
Submitted (02-NOV-1993) Blochemistry Dept, Dartmouth Medical
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                                                                                    3 (bases 1 to 4011)
Chang, C.C. and Chang, T.Y.
Direct Submission
Submission
Submitted (20-May-1999) Blochemistry Dept, Dartmouth Medischool, Hanover, NH 03755, USA
Sequence update by submitter
On May 20, 1999 this sequence version replaced gi:409203.
Location/Qualifiers
1. 4011
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                                                                                                                                                                                                                  /organism="Homo sapiens"
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/cell_line="THP-1 (Phorbol ester activated)"
/cell_type="macrophage"
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Pred. No. 2.4e-71;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
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GRIVLERNILGYRFGKLPPVIWTWARMFISTLSIPYELFQRAHGFSKRFNDFLYSLS
HGFFFLVPQLGILGFVPTYVLTLPPASRFIVILEQIRMWRAHSTVRENVENN
ARREKSSTVPVPTYNQYIFELFAPTLIYRDSYPTPTVRNGGYNAVQFLQVFGCLFYVY
YFFRICAPPFINTQEPFSARVLVLCVFNSILPGVLMLFIFFFAFLHGWLNAFAEML
RRGDRAFYNDWMYSTSYSNYYRTWNVVVHDWLYYYAYRDLMFFSKRFKSAAMLAVFA
LSAVVHEVALAVCLSYFYPVLFVLFREFGMARNFTYNDSRKRPIWNIMVWASLFLGHG
VILCFYSQEWYARQHCPLKNPFFLDYVRPRSWTCQYVF"
1 (bases 1 to 3024)
Cao.G., Goldstein, J.L. and Brown, M.S.
Complementation of mutation in acyl-CoA:cholesterol acyltransferase (AAAT) fails to restore sterol regulation in ACAT-defective sterol-resistant hamster cells J. Biol. Chem. 271 (24), 14642-14648 (1996).
                                                                                                                                        Cao,G., Brown,M.S. and Goldstein,J.L.
Direct Submission
Submitted (26-JAN-1996) Guoqing Cao, Molecular Genetics, University
of Texas Southwestern, 5323 Harry Hines Blvd., Dallas, TX 75235,
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Pred. No. 3.6e-71;
0; Mismatches 516;
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/organism="Cricetulus griseus"
/db_xref="taxon:10029"
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674 c 651 g 97
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58.5%;
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AF354622
Gorilla gorilla cholesterol acyltransferase 1 (ACAI) mRNA, partial
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Gorilla gorilla
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Gorilla.
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                                           949 ATGTACCTAGAGTACTAAATGCCGCCAAGGAAAAATCAAGCACAGTTCCAGTACCCACAG
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---CAGGCCCCCAGTT
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Stauffer, R.L., Walker, A., Ryder, O.A., Lyons-Weiler, M. and
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  CTGTGCCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGATC--
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YTLPPASRFTIIFEOIRFVWKAHSFYRENVPRYLNSAKEKSSTVPIPTVNQYLYFLFA
PLIYRDSYPRNPTVRWGYVAMKFQOYGGCFFVYYYIFEKLAPLFRINKQEPFSSRV
LVLCVFNSILEGVYLLFLTFFFEHLWMLNAFPEMLRFGDRRFYKDWNNSTSYSNYYR
WNVVVHDWLYYYAYKDFLWFFSKRFKSAAMLAVFAVSAVVHEYALAVCLSFFYPVLFV
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HFDDFVTNLIEKSASLDNGGCALTTFSVLEGEKNNHRAKDLRAPPEQGKIFIARRSLL
DELLEVDHIRTIYHMFIALLILFILSTLVVDYIDEGRLVLEFSLLSYAFGKFPTVVWT
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                                                                                                       of Biology, The Pennsylvania
University Park, PA 16802, USA
         paleontological
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           constraints on
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/organism="Gorilla gorilla"
/db_xref="taxon:9593"
/cell_type="cultured fibroblast cells"
<1. .1528
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                                                                                        Direct Submission
Submitted (27-FEB-2001) Department
State University, 208 Mueller Lab,
Location/Qualiflers
           ape molecular clocks and
                                Hered. 92 (6), 469-474 (2001)
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/db_xref="GI:18028942"
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Hedges, S.B.
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les 754; Conserv
Hedges, S.B.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BC028940
BC028940.1 GI:20809439
MGC.
                                                                                                                                                                                                                                                                                               921 TITICIALGERCTACATCTITGAAGGCITTGIGCCCCCTGTITCGGAATAICAAA
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                                                                                                              862 AGGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGT
                                                                                                                                                                                                        922 GIGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGC
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749 CTGTGCCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGGATCCAGGCCCCCAGTTTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1042 ATCTTCATGCTGCTGCTCATCTTCTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCC
                                                                                       G-----CTACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCT
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RSLFHGFLFMIFQIGVLGFGPTYVVLAYTLPPASRFIIIFEQIRFVNKAHSFVRENV
RVLNGAKEKSSTVPIPTVNQYLYFLFAFTLIYBDSYRNHYVNKGYVMKFAVVFGCF
RVLYYIFERLCAPLFRNIKOGPFSARVLVLCVFNSILPGVLILFLTFFRAFLHWLNA
AEMLREGDRMFYKDWNNSTSYSORYRTWNVVHDWLYYAYKDFLMFFSKRFKSAAML
AVFAVSAVVHEYALAVCLSFFYPVLEVLFWFFGMAFFINNDSRKKFIMWTSLF
                                                                                                                                                                                                                                                                                                                                       Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRMK Plate: 42 Row: i Column: 23 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="sterol O-acyltransferase (acyl-Coenzyme A:
cholesterol acyltransferase) 1"
protein_id="AAH28940.1"
/db.xef="GI:20809440"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KQLIAKKIKLTAEAEELKPFFWKEVGSHFDDFVTNLIEKSASLDNGGCALTTFSVLEG
EKNNHRAKDLRAPPEQGKIFIARRSLLDELLEVDHIRTIYHMFIALLILFILSTLVVD
Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                      X., Hulyk, S.W., Hale, S.M., S., Martin, R.G., Muzny, D.M.
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                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome
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/tissue_type="Placenta, choriocarcinoma"
/clone=lib="NHLMGC_10"
/lab_host="PH10B"
/note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 405.6; DB 9;
Pred. No. 5.1e-71;
0; Mismatches 509;
                                                                                                                                                                                                    Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                       Contact: amgébem.tmc.edu
domaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Covis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="LocusID:6646"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
1. .3407
                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                       CICATCCGCTGATCTCTTTCTTCATGATTTCATCATCTTCAGATTGGAG
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CCACCCTGTTGGCGCCGTACCAGGCCCTACGGCTGTGGGCCCAGGGGCACCTGGACGCAGG
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                                                     644 CTACATTTTCAGTTCCCTATTTTCTGTTTCAACATTGGGCCACTGGCTATAGCAAGAGTT
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                       PAT
                                                                                                                                                                                                                                   Length 4011;
                                                                                                                 1 (bases 1 to 4011)
ChangyT.Y. and Chang,C.C.Y.
Acyl coenzyme A:cholesterol acyltransferase (ACAT)
Patent: US 5834283-A 3 10-NOV-1998;
                       linear
                                                                                                                                                                                                                                25.9%; Score 405.6; DB 6; 58.9%; Pred. No. 5e-71; tive 0; Mismatches 509;
                  Sequence 3 from patent US 5834283.
AR053912
AR053912.1 GI:5978774
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                                                                                                                                                               Location/Qualifiers
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              1042 ATCTTCATGCTGCTGCTCATCTTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCC
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Search completed: April 30, 2003, 14:09:08 Job time : 2957 secs

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Human acylcoenzyme Human cDNA SEQ ID Human acylcoenzyme Human acyl CoA:cho DNA encoding a pro Human ACAT Related

cDNA encoding nove

Drosophila melanog Acetyl coenzyme A:

melanog

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Minimum DB seq Maximum DB seq

Database

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Human ACAT Related Gene Product 2 ARGP2 coding sequence
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AAX30335
AAA88846
AAZ45385
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AAA48942
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                                                     April 30, 2003, 12:17:55 ; Search time 262 Seconds (without alignments) 13486.204 Million cell updates/sec
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1569
1 atggagccagggggggccg..........cttggtcctgccatacctag
       GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                2185239 seqs, 1125999159 residues
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Listing first 45 summaries
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s derived by analysis of
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Human secreted proHuman ovarian canc
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Acyl-COA:cholester
Rat sterol acyltra
Corn diacy1glycero
Chemically pretrea
Wheat diacy1glycero
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Soybean diacylglyc Human immune/haema M. alpina acyl CoA Acyl-CoA:cholester Mortierella alpina

Gene encoding a su Arabidopsis diacyl A. thaliana diacyl Arabidopsis acyl C

Acyl-CoA:cholester

Human; ACAT Related Gene Product 2; ARGP2; enzyme; acyl Coenzyme A-cholesterol acyltransferase 1; ACAT1; ACAT2; sterol esterification; lipid homeostasis; diacylglycerol acyltransferase; Location/Qualiflers 52..1620 /*tag= a /product= "Human ARGP2" (UYCO) UNIV COLUMBIA NEW YORK 98US-0165042 98US-0165042 01-OCT-1998; 01-OCT-1998; JS6100077-A. 38-AUG-2000

Human ACAT Related Human acyl CoA:cho Mouse acyl CoA:cho

Description

DB

Length

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Human acylcoenzyme Acetyl coenzyme A: Human acylcoenzyme Acylcoenzyme A:cho Drosophila melanog

AAA76170
AA257360
AA257359
AAV01534
AAQ63212
AAQ63212
AAV01536
AAV01545

2040 1509 1607 1082 4011 3649 3650 455

99.7 90.9 70.9 41.1 26.0 25.7 25.1 112.2

1564.2 1425.8 1112.4 645 407.2 394.6 191.8

Human acyl-coenzym

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                                                                                                                  The enzyme acyl Coenzyme A-cholesterol acyltransferase 1 (ACATI) mediates sterol esterification, an important component of intracellular lipid homeostasis. The present sequence is the coding sequence of human ACAT Related Gene Product 2 (ARGP2/ACAT2). The enzyme encoded by the present sequence is a diacylglycerol acyltransferase (DGAT). ARGP2 esterifies cholesterol. Also, the activity of ARGP2 is relatively resistant to histidine active site modifier. ARGP2 is therefore a tissue specific sterol esterification enzyme.
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                                                    New nucleic acid encoding a human diacylglycerol acyltransferase, useful for treating hyperlipidemia, atherosclerosis, heart disease, other diseases associated with an imbalance of triglyceride levels
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acyltransferase designated ACAT-2. ACAT-2 polypeptides can be
acyltransferase designated ACAT-2. ACAT-2 polypeptides can be
administered therapeutically, especially by expressing encoding
complynucleotides, to treat individuals in need of ACAT-2 polypeptide.
CC polynucleotides, to treat individuals in need of ACAT-2 polypeptide.
CC polynucleotides administered to treat disease conditions
associated with elevated cholesterol ester levels e.g.
Chypertriglyceridaemia or hyperlipidaemia (including
hypertriglyceridaemia), since ACAT-2 catalyses the esterification of
cholesterol with fatty acyl CoA substrates. The polypeptides can also
cobe used to diagnose diseases related to polypeptide expression or
activity, by analysing for polypeptide presence or amount in a sample.
They are useful to screen for compounds inhibiting or activating the
polypeptide, which can be included in pharmaceutical compositions and
administered therapeutically to treat conditions associated with ACAT-2;
inhibitory agents can especially be used to inhibit ACAT-2 activity,
cinhibit ACAT-2 and not prior art ACAT-1.
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antilipaemic; hypercholesterolaemia; hypertriglyceridaemia;
hyperlipidaemia; ss.
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                                                                              /*tag= a
/product= "ACAT-2"
/transl_except= (pos:571..573,aa:Xaa)
/note= "Xaa is unspecified"
                                                                                                                                                                                                                                                                   SK;
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Best Local Similarity 95.6%;
Matches 1500; Conservative
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P-PSDB; AAY67953.
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                                                                   CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGGAGGTGCAGCATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptide, useful to treat conditions associated with elevated sterol ester levels e.g. hypercholesterolemia
                                                                                                              GTCCTGGGGTTCTTCTATCCCGTCATGCTGATACTCTTCCTTGTCATTGAGGAATGTTG
                                          AACTTCATGATGCATGACCAGCGCACCGGCCCGGCATGGAACGTGCTGATGTGGACCATG
                                                                        CTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGG
                                                                                                                                                                                                                                                                                                               Mouse; acyl CoA:cholesterol acyltransferase; ACAT-2; diagnosis; antilipaemic; hypercholesterolaemia; hypertriglyceridaemia;
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                                                                                                                                 Length 1607;
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                                                                                                                               Score 1112.4; DB 21; Lengt
Pred. No. 3.7e-267;
0; Mismatches 247; Indels
                                                                                                     Sequence 1607 BP; 299 A; 466 C; 456 G; 385 T; 1 other;
                                                                           inhibit ACAT-2 and not prior art ACAT-1.
                                                                                                                         70.9%; Scc.
83.2%; Pred
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                                                                                                                                                                 Conservative
                                                                                                                                                   Similarity
                                                                                                                                                                 Matches 1295;
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                                                                           1071 GGGCCAGGCATCTTCATGCTGCTCCTCATCTTCTCGCCTTCCTGCACTGCTGGCTCAAC
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913 CTGGGATGTGTGTCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTTCCTGTCTTTGCC
                                                                                                                                            ACAT related gene product 2; human; sterol esterification;
Inhibitor; atherosclerosis; hyperlipidaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human acylcoenzyme A:cholesterol acyltransferase III DNA
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ACAT related gene product 2; human; sterol esterificati
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This isolated nucleic acid molecule encodes human acylcoenzyme A:cholesterol acyltransferase III (see AAW3407), or ACAT related gene product 2 (ARGP-2), whose expression appears to be restricted to the foetal liver, suggesting it to have a role in lipid metabolism during development. It was identified following database searching for human ACAT-related sequences and use of PCR and RACE to obtain full-length sequences. An isolated nucleic acid (see AAV01533) for human ARGP-1 (see AAW43406) was also identified. Also claimed are host vector systems for production of ARGP-1 and ARGP-1 colling and transgenic non-human mammals. ARGP-1 and ARGP-1 collingian imbalance in sterol levels due to a defect in esterification of sterol. A claimed oligonocleckide capable of specifically carefold. A calmed oligonocleckide capable of specifically collinging to a unique sequence of nucleotides in the isolated nucleic acid molecule, or a vector expressing the oligonoclectide. Can be used to inhibit wild-type ARGP-1 or ARGP-2. The wild-type enzymes can be used to identify an inhibitor, useful in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 961 CCTGTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGTGCCCTTGGTGCTCTTATC 1020
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treatment of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treatment of atherosclerosis or hyperlipidaemia.
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                                                                                                                                                                                                                                                                         III - useful to identify inhibitors for
atherosclerosis or hyperlipidaemia
                                                                                                                                                                                                                                        encoding acylcoenzyme A: cholesterol
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(UYCO ) UNIV COLUMBIA NEW
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Matches 654; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
1397..3049
/*tag= a
/*reduct Acetyl CoA: cholesterol acetyltransferas
3385..3389
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                                                                                                                                         CTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGGGG
                                                                                                                   CACTGCCCCTTACCCCAGGCAACTTTCTGGGGGCTGGTGACACCTCGATCTTGGTCCTGC
                                                                      CTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acetyl coenzyme A; cholesterol acetyltransferase; ACAT; disease; diagnosis; detection; screening; treatment; prophylaxis; hypercholesterolaemia; atherosclerosis; antisense; probe; identification; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
/note= "Putative polyadenylation signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coenzyme A: cholesterol acetyltransferase (ACAT).
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93US-0121057.
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10-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         467 TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGT
                                                                                                                             26;
                                                                                      4011;
                                                                                    Length
  Ϋ́
                                                                                Score 407.2; DB 15; Length.
Pred. No. 2.8e-91;
0; Mismatches 508; Indels
                                         Sequence 4011 BP; 1056 A; 793 C; 839 G; 1323 T; 0 other;
This sequence is a human ACAT cDNA sequence designated
                                                                                      26.0%;
59.0%;
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Matches 768; Conservative
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                                                                                                                                                                                                      CAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGGCACTGCCCCTTACCCCCAGGCA 1521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This nucleic acid molecule encodes human acylcoenzyme A:cholesterol acyltransferase (see AAW43409), or ACAT I. The invention relates to isolated nucleic acids (see AAV01533-35) coding for human and mouse acylcoenzyme A:cholesterol acyltransferase II and III (see AAW443406-08), also designated ACAT related gene products (ARGP) I and 2. These can be used to identify inhibitors useful in the treatment of atherosclerosis and hyperlipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acylcoenzyme A:cholesterol acyltransferase; ACAT I;
ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
inhibitor; atherosclerosis; hyperlipidaemia; human; ss.
2696 AAGGACTTTCTCTGGTTTTTCTCCAAGAGATTCAAATCTGCTGCCATGTTAGCTGTTTTT
                                                                                                                                                                2876 CGGAAAAAGCCGATTTGGAATGTTCTGATGTGGACTTCTCTTTTCTTGGGCAATGGAGTC
                                                                 CGCACCGGCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATC
                                        CTGGTCTCCGCAGTGGCCCATGAGTATCTTCTGCTTCGTCCTGGGGGTTCTTCTATCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Human acylcoenzyme A:cholesterol acyltransferase (ACAT
                                                                                                                                                                                                                                                          ACTITCIGGGGCTGGTGACACCTCGATCTTGGTCCTGCCAT 1563
                                                                                                                                                                                                                                                                         DNA encoding acylcoenzyme A: cholesterol
III - useful to identify inhibitors for
atherosclerosis or hyperlipidaemia
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P-PSDB; AAW43409.
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                                                                                      CATCCCTGGGGAAACAGAAGTTTTCATCATCGCAAGTCCCTGCTTGATGAGCTGATGG
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                                                       26;
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Sequence 3649 BP; 929 A; 749 C; 781 G; 1190 T; 0 other;
                                                        0; Mismatches 510;
                             Score 404; DB 19;
Pred. No. 1.7e-90;
                             25.7%;
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                                                                                                                                                           This DNA sequence includes a coding region for human macrophage acyl-coenzyme A:cholesterol acyltransferase I (hACAT) (see AAW38416) It has been used to search for homologous yeast genes (see AAT96369 and AAT96370) and subsequently to identify an additional human isoform (see AAW38421). A novel claimed expression vector (I)
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          1282 CIGGICICCGCAGIGGCCCAIGAGIAIAICIICIGCTICGICCIGGGGITCTICIAICCC .
                       CGCACCGGCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATC
                                                                                                                                                1462 CAGGICAGCCIGIACIGCCAGGAGIGGIACGCACGGCGGCACIGCCCCTIACCCCAGGCA
                                                        GTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAG
                                                                                                              Location/Qualifiers
1397..3050
1497..3050
//tradsl_except= (pos:2492..2495, aa:Val)
/rote= "this codon has an apparent 1 nuclectide insertion, which alters the reading frame"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast acyl:coenzyme A:cholesterol acyl:transferase related and II - useful to identify inhibitor for treatment of hyperlipidaemia, arteriosclerosis and fungal invasion
                                                                                                                                                                                                                                                                                                                                                            Acyl-coenzyme A: cholesterol acyltransferase I; ACAT; huma: sterol; esterification; arteriosclerosis; hyperlipidaemia; antifungal; fungicide; ss.
                                                                                                                                                                                                                                                                                                                                         Human acyl-coenzyme A:cholesterol acyltransferase I DNA
                                                                                                                                                                                                        ACTITCIGGGGGCTGGTGACACCTCGATCTTGGTCCTGCCAT
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                                                                                                                                                                                                                                                                          DNA; 3650
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                                                                                                                                                                                                                                                                        AAT96368 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                     21-MAY-1998
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                                                                                                                                                                                                                                                                                              AAT96368;
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                                                                                                      1402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1737 CACCTCCAGAACAAGGAAAGATTTTATTGCAAGGCGCTCTCTTAGATGAACTGCTTG 1796
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                                                                                                                                                                                                                                                                                                                                                                           AGGIGCAGCATTICCGCACCATCIACCACATGITCATCGCTGGCCTGTGTGTTCATCA 406
                                                                                                                                                                                                                                                                                               287 CATCCCTGGGGAAACAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGGCTGATGG 346
comprises an isolated nucleic acid molecule encoding yeast wild type acyl-coenzyme A:cholesterol acyltransferase 1 (ARE1) (see AAW38417) or 2 (ARE2) (see AAW38418) operatively linked to a promoter. The vector and a claimed host-vector system can be used for the recombinant production of ARE1 or ARE2. The products can be used to identify novel ARE1 or ARE2 inhibitors. ARE2 inhibitors can be used to treat arteriosclerosis or hyperlipidaemia, as well as to inhibit fungal growth or to treat fungal invasion (claimed).
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                  CCACCCTGTTGGCGCCGTACCAGGCCTTACGGCTGTGGGCCAGGGGCACCTGGACGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           749 CTGTGCCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGATCCAGGCCCCCAGTTTCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2217 ACGIGCCTCGGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCAATACCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       809 G-----CTACCICTACTICCTCTTCTGCCCAACACTCTACAGGGAGACTIACCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGT
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                                                                                                                                                                                                                         DB 19; Length 3650;
                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                Sequence 3650 BP; 929 A; 750 C; 781 G; 1190 T; 0 other;
                                                                                                                                                                                                                       Score 394.6; DB 19;
Pred. No. 3.7e-88;
0; Mismatches 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25.1%;
58.9%;
                                                                                                                                                                                                                                                Best Local Similarity 58.9
Matches 767; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           647 TCC-----
                                                                                                                                                                                                                             Query Match
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relates to isolated nucleic acids (see AAV01533-35) coding for human and mouse acylcoenzyme A:cholesterol acyltransferase II and III (see AAW43406-08), also designated ACAT related gene products (ARGP) 1 and 2. These can be used to identify inhibitors useful in the treatment of atherosclerosis and hyperlipidaemia.
                                                                                                                                           Sequence 455 BP; 95 A; 121 C; 123 G; 116 T; 0 other;
                                                                                                                                                                                         DB 19;
                                                                                                                                                                                      Score 191.8; DB 1
Pred. No. 5.8e-38;
                                                                                                                                                                                                                                    0; Mismatches
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99.0%;
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11-JUL-2000; 2000US-0614150.
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                                                                                                                                                                                                                                    Matches 193; Conservative
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pharmaceutical; gene; ss
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                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                      Query Match
Best Local S
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  2576 TGAGATGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTGGTGGAACTCCACGTCATA 2635
                                                                                                                                                                                                                                                                                                                             CGTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCA 1400
                                                                        2636 CTCCAACTATTATAGAACCTGGAATGTGGTGGTCCATGACTGGCTATATTACTATGCTTA
                                                                                                                                                                   2696 CAAGGACTTTCTTTTTTTCTCCAAGAGTTCAAATCTGCTGCCATGTTAGCTGTCTT
                                                                                                                                                                                                                                 1281 CCTGGTCTCCGCAGTGGCCCATGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCC
                                                                                                                                                                                                                                                            TGCTGTATCTGCTGTAGTACACGAATATGCCTTGGCTGTTTGCTTGAGCTTTTTTCTATCC
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                                                                                                                                        1221 TCAGGATGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTGTT
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                                                  CTCCAACTACCGCACTTGGAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTA
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treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acylcoenzyme A:cholesterol acyltransferase partial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTITCIGGGGGCTGGTGACACCTCGATCTTGGTCCTGCCAT 1563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2996 CACATTTTTGGATTATGTCCGGCCACGTTCCTGGACTTGTCGT 3038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding acylcoenzyme A: cholesterol
III - useful to identify inhibitors for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 70; 121pp; English
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Length 455;
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Claim 1; SEQ
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                                                                                                                                                                                                                                        CAAGAACTTTGCCCAGGCCCTGGGATGTGTGCTCTATGCCTGCTTCATCCTGGGCCGCCT
                                                                                    Length 1885;
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                                                            Sequence 1885 BP; 410 A; 514 C; 504 G; 457 T; 0 other;
                                                                                  ; DB 23;
8.5e-33;
ches 380;
 (ABB57737-ABB72072).
The sequence data for this patent did not form The sequence data for this patent did not form escification, but was obtained in electronic fat ftp.wipo.int/pub/published_pct_sequences.
                                                                                                    Pred. No. 8.5e
0; Mismatches
                                                                                     11.0%; Score 172; 51.9%; Pred. No. 8
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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Drosophila melanogaster expressed polynucleotide SEQ ID NO 41564
                                                     developmental biology; cell signalling; insecticide
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Pred. No. 9.6e-33;
0; Mismatches 380;
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nilarity 51.9%;
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2000US-0614150.
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                                                                                        pharmaceutical; gene; ss
                                                                                                                                                Drosophila melanogaster.
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is
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CCGGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACGTGGTGGT
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                545 CAAGGACTGGTGGACGTCGCACATTACGATGGCTACTACAGAAACTGGAATGTCGTCGT
                                            CCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGGC
                                                       Claim 1; SEQ ID NO 35756; 21pp + Sequence Listing; English.
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P-PSDB; ABB69655.
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(ABBS7737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo int/pub/published_pct_sequences.
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                                                                                                                                                                                                                              Gaps
useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical frugs. The invention discloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                                                                                                                                                                                                                              774 ACGAGGTGAGGGGATCCAGGCCCCCAGTTTCTCCAGCTACCTCTACTTCCTCTTCTGCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCTCTCTGATCCTGGGAAATGCCACGCTGATCTCACTATACGCCATGGAGCATTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCCACGAGCACTTCGGACAGTACGGACTGGAACCAATGGGACCCTCCCAGCTGATCCT
                                                                                                                                                                                                                              3;
                                                                                                                                                                                              Length 4,260;
                                                                                                                                                                                                                              Indels
                                                                                                                                                              0 other;
                                                                                                                                                                                            Score 172; DB 23;
Pred. No. 1.2e-32;
0; Mismatches 380;
                                                                                                                                                                Sequence 4260 BP; 1152 A; 961 C; 962 G; 1185 T;
                                                                                                                                                                                              Query Match
Best Local Similarity 51.9%;
Matches 413; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 AGGIGCAGCAITICCGCACCAICTACCACAIGITCAICGCIGGCCIGIGIGICTTCAICA 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the design of drugs serving as specific ACAT inhibitors, desirable for the prevention and/or treatment of human hypercholesterolaemia and human atherosclerosis. It also allows the design of antisense DNAs or RNAs to inhibit ACAT prodction, or probes to identify different forms of human ACAT or ACAT from different animal species. This sequence is a human ACAT CDNA clone designated Cl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TCAGCACCCTGGCCATCGACTTCATTGATGAGGGCAGGCTGCTGCTGG--AGTTTGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The acetyl coenzyme A: cholesterol acetyl-transferase (ACAT) gene sequence enables the screening of human populations for abnormal human ACAT activities for disease diagnosis. It provides information concerning the catalytic mechanism of ACAT and allows
                                                                                                                                                                                                                                                     ACAT; disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acetyl coenzyme A: cholesterol acetyl-transferase and nucleic acid sequence encoding it - used to correct enzyme deficiencies and screen for enzyme inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 53.1%; Pred. No. 1.4e-23; Donservative 0; Mismatches 324; Indels 21;
                                                                                                                                                                                                                                                  Acetyl coenzyme A; cholesterol acetyltransferase; ACAT; diagnosis; detection; screening; treatment; prophylaxis; hypercholesterolaemia; atherosclerosis; antisense; probe;
                                                                                                                                                                                                          Acetyl coenzyme A: cholesterol acetyltransferase (ACAT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 996 BP; 258 A; 219 C; 207 G; 312 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Figure 3; 52pp; English.
                                                        AAQ63210 standard; cDNA; 996 BP.
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93US-0121057
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                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chang T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1994-151312/18.
                                                                                                                                                                                                                                                                                                                                  identification; ss.
                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-OCT-1992;
10-SEP-1993;
                                                                                                                                                            03-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                           AAQ63210;
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ACAT related gene product 1; ARGP-1; ARP-2; sterol esterification;
inhibitor; atherosclerosis; hyperlipidaemia; human; ss.
                                                                                                                                                                                                                                               CGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGTGTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          562 GITCTCATCCGCTGATCCGTTCTTTTCCATGGCTTTCTTTTCATGATCTTCCAGATTG
                                                                                                                                                                                                                GTGCCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGATCCAGGCC-----CCCCAGTTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TGCGCGCTGCCGGTCCACGTGGCCGTGGAGCATCAGCTCCCGCCGGCCTCCCGTTGT
                                                                                                                                                              622 GAGIICTAGGIIITIGGACCAACATAIGIIGIGIIAGCAIAICCIGCCACCAGCIICCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human acylcoenzyme A:cholesterol acyltransferase II (ACAT II) DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                 806 CCAGCTACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding acylcoenzyme A: cholesterol acyltransferase II or
III - useful to identify inhibitors for treatment of
atherosclerosis or hyperlipidaemia
584 AGGCGACGGGCCTGGGCTGTGCGCTTTTAGCCGCCCACGCCGTGGTGCTC--
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2000US-2166479-
2000US-2168809-
2000US-2174879-
2000US-2209649-
2000US-2209649-
2000US-2245189-
2000US-2245189-
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2000US-2252679-
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2000US-226868P
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                                                                                                                                                                                                                                                                                                                                                                                   GGGTAGCCATGCTGGGTGTTCCTGGTCTCCGCAGTGGCCCATGAGTATATCTTCTGCT 1318
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                                                                                                                                                                                                                                                                                                                                                                                                       416 GGATGGCCAGGACAGGGGTGTTCCTGGCCTTGGCTTTCTTCCACGAGTACCTGGTGAGCG 475
                               This nucleic acid molecule encodes human acylcoenzyme A:cholesterol acyltransferase I (see AAW43412), or ACAT II. The invention relates to isolated nucleic acids (see AAV01533-35) coding for human and mouse acylcoenzyme A:cholesterol acyltransferase II and III (see AAW43406-08), also designated ACAT related gene products (ARGP) I and 2. These can be used to identify inhibitors useful in the treatment of atherosclerosis and hyperlipidaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation; ss.
                                                                                                                                                                        Gaps
                                                                                                                                                                                                          302 ACTGGTGGAACTCCGAGTCTGTCACCTACTTCTGGCAGAACTGGAACATCCCTGTGCACA
                                                                                                                                                                                                                                                                                                                                                           362 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT
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9
                                                                                                                                              6.1%; Score 95; DB 19; Length 983; 58.7%; Pred. No. 1e-13; tive 0; Mismatches 125; Indels
                                                                                                                          Sequence 983 BP; 193 A; 314 C; 263 G; 213 T; 0 other;
          Disclosure; Page 68; 121pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABA06413 standard; cDNA; 993
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2000US-190076P.
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Matches 186; Conservative
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18-APR-2000;
19-MAY-2000;
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04-FEB-2000;
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02-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                   546 GGATGGCCAGGACAGGGGTGTTCCTGGCCTTCGTCTCCACGAGTACCTGGTGAGCG 487
                                                                                                                                                 DNA encoding acylcoenzyme A: cholesterol acyltransferase II or
III - useful to identify inhibitors for treatment of
atherosclerosis or hyperlipidaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acylcoenzyme A:cholesterol acyltransferase II; ARGP-1; ACAT related gene product 1; human; sterol esterification; inhibitor; atherosclerosis; hyperlipidaemia; ss.
                                                           Query Match
6.1%; Score 95; DB 22; Length 99
Best Local Similarity 58.7%; Pred. No. 1e-13;
Matches 186; Conservative 0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human acylcoenzyme A:cholesterol acyltransferase II DNA
                              Sequence 993 BP; 218 A; 260 C; 328 G; 186 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers 1.1224
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is a cDNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO: 79; 859pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
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P-PSDB; ABB10191.
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Archolesterol anyltransferase II (see AAW43406), or ACAT related gene product 1 (ARGP-1), that is expressed at high levels in intestine and is a candidate for sterol esterification in these tissues. It was identified following database searching for human ACAT-related sequences and use of PCR and RACE to obtain full-length sequences. An isolated nucleic acid (see AAW01534) for human ARGP-2 (see AAW43407) was also identified. Also claimed are host vector systems for production of ARGP polypeptides, and transgenic non-human mammals. ARGP-1 and ARGP-2 nucleic acids can be used to diagnose or treat a sterol esterification. A claimed oligonucleotide capable of specifically hybridising to a unique sequence of nucleotides in the isolated nucleic acid molecule, or a vector expressing the claimed acid molecule, or a vector expressing the claimed the unique type enzymes can be used to inhibit wild-type ARGP-1 or ARGP-2. The wild-type enzymes can be used to identify an inhibitor, useful in the treatment of atherosclerosis or hyperlipidaemia.
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                             This isolated nucleic acid molecule encodes human acylcoenzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.1%; Score 95; DB 19; Length 1521; Best Local Similarity 58.7%; Pred. No. 1.2e-13; Matches 186; Conservative 0; Mismatches 125; Indels
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Patent No. 6100077
Patent No. 6100077
Patent No. 6100077
APPLICANT: Sturley, Stephen L.
APPLICANT: Oelkers, Peter
TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
TITLE OF INVENTION: ACTLTRANSFERASE
FILE REFERENCE: 0575/56331
CURRENT APPLICATION NUMBER: US/09/165,042
CURRENT APPLICATION NUMBER: US/09/165,042
SOFTWARE: PATENT OF DATE: 1998-10-01
NUMBER OF SOF DI NOS: 32
SOFTWARE: PATENTIN VET. 2.0
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                    US-08-439-009A-3
PCT-US92-06840-1
US-09-007-005-17
US-09-24-796-17
US-08-199-926-2
US-09-109-926-2
US-09-114-085-3
US-08-125-468-1
US-08-125-468-1
US-08-125-468-1
US-08-105-33-2
US-09-105-537-2
US-09-105-537-3
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Pred. No. 0;
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CACTGCCCCTTACCCCAGGCAACTTTCTGGGGGCTGGTGACACCTCGATCTTGGTCCTGC
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Pred. No. 1.16
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ATTORNEY/AGENT INFORMATION:
NAME: LAWORT HAMMITTE, ANN.
REGISTRATION NUMBER: 34,858
REFERENCE/DOCKET NUMBER: DCI-033CP
TELECOMUNICATION INFORMATION:
TELEPHONE: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ACYL COENXYME A:
TITLE OF INVENTION: ACYLFRANSFERASE (
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                  510
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,057
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: LAHIVE & COCKFIELD STREET: 60 STATE STREET, SUITE
                                                                                                                                                                                                                                                                                                 APPLICANT: CHANG, TA-YUAN
APPLICANT: CHANG, CATHERINE C. Y.
                                                                                                                                                                                                                                  Sequence 3, Application US/08121057 Patent No. 5484727 GENERAL INFORMATION:
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58.9%;
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LENGTH: 4011 base pairs
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                          Massachusetts
                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                     CITY: Boston
STATE: Massac
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; LOCATION:
US-08-509-187D-3
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                                                                                                                                                                                                                                                                                                             COUNTRY:
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1917 TGTCTTATGCTTTTGGCAAATTTCCTACCGTTGTTTGGACCTGGTGGATCATGTTCCTGT 1976
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                                          CCACCCTGTTGGCGCCCGTACCAGGCCCTACGGCTGTGGGCCCAGGGGCCACCTGGACGCAGG
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1917 IGTCTTATGCTTTTGGCAAATTTCCTACCGTTGTTTGGACCTGGTGGATCATGTTCCTGT 1976
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                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/08/509,187D
FILING DATE: 31-JUL-1995
                                                                              Catherine C. Cholesterol
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                                                                      APPLICANT: Chang, Ta-Yuan and Chang, TITLE OF INVENTION: ACYL Coenzyme A: NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: AADDRESSEE: LAHIVE & COCKFIELD, LLP STREET: 28 State Street
Sequence 3, Application US/08509187D Patent No. 5834283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Lamport Hammitte, REGISTRATION NUMBER: 34
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Sequence 3, Application US/09121396 Patent No. 5968749 GENERAL INFORMATION:

RESULT 4 US-09-121-396-3

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Pred. No. 1.1e-94;
0; Mismatches 509;
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APPLICANT: CHANG, TA-YUAN
APPLICANT: CHANG, CATHERINE C. Y.
TITLE OF INVENTION: ACYL COENZYME A: TITLE OF INVENTION: ACYLTRANSFERASE (** NUMBER** OF SEQUENCES: 9
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,396
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/509,187
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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58.9%;
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ATTORNEY/AGENT INFORMATION:
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Matches 767; Conservative
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MEDIUM TYPE: Floppy
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                                                                     2217 ACGTGCCTCGGGTACTAAAT-TCAGCTAAGGAGAAATCAAGCACTGTTCCAATACCTACA
                                                                                                                 AGGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCTGGGATGT
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
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PCT-US93-09704A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 405.6; DB 5;
Pred. No. 1.1e-94;
0; Mismatches 509;
                                                                                                      NO. 959,950
                                                                                                                                        121,057
                   PCT/US93/09704A
                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: DCI-033CP TELECOMMUNICATION INFORMATION:
                                                                                                                                                              FILING DATE: September 10, 1993
ATTORNEY AGBNI INFORMATION:
NAME: LAMPORT HAMMITTE, ANN.
REGISTRATION NUMBER: 34,858
                                                                            PRIOR APPLICATION DATA:
PAPLICATION NUMBER: 0.5. SER.
FILING DATE: October 14, 1992
APPLICATION NUMBER: U.S. SER.
                                       October 12, 1993
                                                                                                                                                                                                   LAMPORT HAMMITTE, ANN. RATION NUMBER: 34,858
                                                                                                                                                                                                                                                                                 TELEPHONE: (617) 227-2700
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 25.9%;
Best Local Similarity 58.9%;
Matches 767; Conservative
                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 4011 base pairs
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCT-US93-09704A-3
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GIGCICITAIGCCIGCTICAICCIGGCCCCCCICIGIGIICCIGICITIGCCAACAIGAGC
                      2456 CAGGAGCCCTTCAGCGCTCGTGTTTAGTTTAACTCCATCTTGCCAGT
                                                                                                                                                            2516 GTGCTGATTCTCTTACTTTTTTTTTTTTCCACTGGCTCAATGCCTTTTGCT
                                                                                                                                                                                                                              TCCAACTACTACCGCACTTGGAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTAT
                                                                                                                                                                                                                                                                                                    2636 TCCAACTATTATAGAACCTGGAATGTGGTGGTCCATGACTGGCTATATTACTATGCTTAC
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                                                                     CGAGAGCCCTTCAGCACCCGTGCCCTGGTGCTCTTATCCTGCATGCCACGTTGCCAGGC
                                                                                                                                        1042 ATCTTCATGCTGCTGCTCTTCTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CHANG, TA-YUAN
APPLICANT: CHANG, CATHERINE C. Y.
TITLE OF INVENTION: ACYL COENZYME A:
"TITLE OF INVENTION: ACYLTRANSFERASE (
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5: LAHIVE & COCKFIELD 60 STATE STREET, SUITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08121057 Patent No. 5484727 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASCII Text
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CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE
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셤 ŏ LAMPORT HAMMITTE, ANN

CLASSIFICATION: 800 ATTORNEY/AGENT INFORMATION:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                347 AGGTGCAGCATTTCCGCACCATCTACCACATGTTCATCGCTGGCCTGTGTGTCTTCATCA 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTG-ATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTC
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                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                    Length 4079;
                                                                                                                                                                                                                                                                                                                 Score 359.8; DB 1;
Pred. No. 6.6e-83;
); Mismatches 502;
                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                            0;
34,858
                REFERENCE/DOCKET NUMBER: DC
TELECOMMUNICATION INFORMATION
TELEPHONE: (617) 227-270
TELEPKS: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                    22.9%;
58.0%;
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 4079 base pairs
                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                           single
REGISTRATION NUMBER:
                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                              , MOLECULE TYPE:
US-08-121-057-2
                                                                                                                                                                                                                                                                                                                                                                 Matches 722;
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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  TGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCA
                                                                                                 2708 ACTATTATAGAACCTGGAATGTGGTGGTCCATGACTGGCTATATTACTATGCTTACAAGG
                                                                                                                                                                                                                                                                     2828 TATCIGCIGIAGIACACGAATAIGCCITGGCIGITIGCTIGAGCTITITCTAICCCGIGC
                                                                                                                                                                                                                                                                                                            TGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGCGCA
                                                                                                                                                                                                                                                                                                                                    1406 CCGGCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                            2648 TGTTACGCTTTGGTGACAGGATGTTCTATAAGGATTGGTGGAACTCCACGTCATACTCCA
                                                                             ACTACTACCGCACTTGGAACGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGG
                                                                                                                                                         ATGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTTTCCTGG
                                                                                                                                                                                           ACTITICICIGGITITICICCAAGAGATICAAATCIGCIGCCAIGITAGCIGICITIGCIG
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Cholesterol Acyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGGCACTGCCCCT 1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/509,187D
FILING DATE: 31-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DCI-033cbdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Chang, Ta-Yuan and Chang, TITLE OF INVENTION: 9 ACYL Coenzyme A: NUMBER OF SEQUENCES: 9 CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD, LLP STREET: 28 STREET: 28 STREET: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08509187D Patent No. 5834283 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Lamport Hammitte, Ann
REGISTRATION NUMBER: 34,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: DC
TELECOMMUNICATION INFORMATION
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 4079 base pairs
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STATE: Massachusetts
COUNTRY: USA
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STRANDEDNESS: single
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                        21;
Length 4079;
                        Indels
                        0; Mismatches 502;
            6.6e-83
  Score 359.8;
Pred. No. 6.66
 22.9%;
58.0%;
                        722; Conservative
            Similarity
  Query Match
           Best Local
Matches 72
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 CCGGCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGG
                                   TGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGCGCA
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                                                                                                                                 TCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGGCACTGCCCCT 1510
                                                                                                                                              3008 TCTGCTTTATTCTCAAGAATGGTATGCACGTCGGCACTGTACCT 3052
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APPLICANT: CHANG, CATHERINE C. Y.
TITLE OF INVENTION: ACYL COENXYME A: CHOLESTEROL.
TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/509,187
FILING DATE: 07/31/95
ATTORNEY/AGENT INFORMATION:
NAME: LAMPORT HAMMITTE, ANN.
REGISTRATION NUMBER: 34,858
REPERBNES/DOCKET NUMBER: DCI-033CPDV
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,396
                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: ASCII Text
                                                                                                                                                                                                                   Sequence 2, Application US/09121396
Patent No. 5968749
                                                                                                                                                                                                                                                                                                                             COCKFIELD
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58.0%;
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                                                                                                                                                                                                                                                                                                               STATE: MAINE & COCKI STREET: 28 STATE STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4079 base pairs
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                             INFORMATION:
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Matches 722;
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                                                  1928 TCAGCACACTTGTAGTAGATTACATTGATGAAGGAAGGCTGGTGCTTGCAAGTTACGCCT 1987
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                                                                                                                                                                                                                        TGTCCACCCTGTTGGCGCCGTACCAGGCCCTACGGCTGTGGGCCCAGGGGCCACCTGGACGC
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TCAGCACCCTGGCCATCGACTTCATTGATGAGGGCAGGCTGCTGCTGG--AGTTTGACCT
                                                                                                          ACTG-ATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTC
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                                                             2228 TTCATCATTATTCGAGCAGATCGTTTTGTAATGAAGGCCCACTCATTTGTCAGAGAAC
                                                                                                                                                                                  806 CCAGCTACCTCTTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCTAGGA
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Patent No. 5484727
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CHANG, TA-YUAN
APPLICANT: CHANG, CATHERINE C. Y.
TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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60 STATE STREET, SUITE 510
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STREET: 60 ST
CITY: BOSTON
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DB 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: U.S. SER. NO. 959,950 FILING DATE: October 14, 1992 APPLICATION NUMBER: U.S. SER. NO. 121,057 FILING DATE: September 10, 1993 ATTORNEY/AGENT INFORMATION: NAME: LAMPORT HAMMITE, ANN REGISTRATION NUMBER: 34,858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                              TITLE OF INVENTION: ACYL COENZYME A: CHOLE TITLE OF INVENTION: ACYLTRANSFERASE (ACAT) NUMBER OF SEQUENCES: 9 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: PCT/US93/09704A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: DCI-033CP TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-2700 TELEPAX: (617) 227-5941 FORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                       Sequence 2, Application PC/TUS9309704A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        October 12, 1993
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                              862 ATCCCACTGTAAGATGGGGGTTATGTTGCTATGAAGTTTGCACAGGTCTTTGGTTGCTTTT 921
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                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chang, Ta-Yuan and Chang, Catherine C.Y.
TITLE OF INVENTION: ACYL Coenzyme A: Cholesterol Acyltransferase
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 8.6%; Score 134.6; DB 2; Length 9 Best Local Similarity 53.1%; Pred. No. 2.6e-25; Matches 390; Conservative 0; Mismatches 324; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                        2: LAHIVE & COCKFIELD, LLP 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/509,187D
FILING DATE: 31-JUL-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release
                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08509187D Patent No. 5834283 GENERAL INFORMATION:
APPLICANT: Chang, Ta-Yuan and Cha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lamport Hammitte, Ann
REGISTRATION NUMBER: 34,858
REFERENCE/DOCKET NUMBER: DCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Massachusetts
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: CDNA US-08-509-187D-1
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                                                                                                                                                                                                                                CLASSIFICATION: 800
ATTORNEY/AGENY INFORMATION:
NAME: LAMPORT HAMMITTE, ANN.
REGISTRATION NUMBER: 34,858
REFERENCE/DOCKET NUMBER: DCI-033CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-2700
TELEPHONE: (617) 227-5541
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                    APPLICATION NUMBER: US/08/121,057 FILING DATE:
                                                                            MEDIUM TYPE: Floppy disk.
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 53.11
Matches 390; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                             SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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; MOLECULE TYPE:
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                     502 TGTCTACATTTTCAGTTCCCTATTTTCTGTTTCAACATTGGCGCACTGGCTATAGCAAGA
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                                                    584 AGGCGACGGCCTGGCCTGTGCGCTTTTAGCCGCCCACGCCGTGGTGCTC-
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APPLICANT: CHANG, TA-YUAN
APPLICANT: CHANG, CATHERINE C. Y.
TITLE OF INVENTION: ACYL COENZYME A: CHOLESTEROL
TITLE OF INVENTION: ACYLTRANSFERASE (ACAT)
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: DCI-033CPDV TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 227-2700
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/509,187
FILING DATE: 07/31/95
ATTONIEY/AGENT INFORMATION:
ATTONIEY/ACTIONIES/ALIANTHE ANN
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/121,396
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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28 STATE STREET
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Patent No. 5968749
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STREET: 28 ST
CITY: BOSTON
STATE: MA
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                                                                                                                                                                                               Length
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                                                                                                                                                                                             Score 134.6; DB 2;
Pred. No. 2.6e-25;
0; Mismatches 324;
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                                                                                                                                                                                             Query Match 8.6%;
Best Local Similarity 53.1%;
Matches 390; Conservative
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 996 base pairs
TYPE: nucleic acid
STRANDENESS: single
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US-09-121-396-1
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TITLE OF INVENTION:
                                                                                                                    linear
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                                                                                                                    TOPOLOGY:
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US-09-126-203A-14

Sequence 14, Application US/09326203A

Sequence 14, Application US/09326203A

Sequence 14, Application US/09326203A

Sequence 14, Application US/09326203A

Sequence 14, Application Wike

Sequence 12, Application Sequence 12, TITLE OF INVENTION: Action NUMBER: 05/09/326, 203A

CURRENT FILING DATE: 1999-06-04

PRIOR PRILING DATE: 1999-06-04

PRIOR FILING DATE: 1998-06-05

PRIOR FILING DATE: 1998-06-11-12
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Pred. No. 4.9e-15;
0; Mismatches 125; Indels
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Best Local Similarity 58.7%;
Matches 186; Conservative
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ORGANISM: Human
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Pred. No. 2.6e-25;
0; Mismatches 324;
                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. SER. NO. 959,950
FILING DATE: OCCODER: 14, 1992
APPLICATION NUMBER: U.S. SER. NO. 121,057
         ACYLTRANSFERASE (ACAT)
                                                                                                                                                                                                                                                                                                                                         FILING DATE: September 10, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LAMPORT HAMMITTE, ANN
REGISTRATION NUMBER: 34,858
REFERENCE/DOCKET NUMBER: DCI-033CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-2700
TELEPHONE: (617) 227-2901
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09704A
FILING DATE: October 12, 1993
                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Best Local Similarity 53.1%;
Matches 390; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 996 base pairs
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EDNESS: single
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STRANDEDNESS:
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1079 ATTGCTGGCTCAACGCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGG 1138
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                                  ; Sequence 2, Application US/09165042
; Batent No. 6100077
; GENERAL INFORMATION;
; APPLICANT: Sturley, Stephen L.
; APPLICANT: Sturley, Stephen L.
; TITLE OF INVENTION: ISOLATION OF A GENE ENCODING DIACYLGLYCEROL
; TITLE OF INVENTION: ACVITANNSFERASE
; FILE REFERENCE: 0575/56331
; CURRENT APPLICATION NUMBER: US/09/165,042
; CURRENT FILING DATE: 1998-10-01
; SOFTWARE: PatentIn Ver. 2.0
; SOFTWARE: PatentIn Ver. 2.0
; SEC ID NO 2
; LEATH: 1976
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 95; DB 3; Length 1976;
Pred. No. 5e-15;
0; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                  6.1%; 58.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.7%
Matches 186; Conservative
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; ORGANISM: Yeast
US-09-165-042-2
RESULT 15
US-09-165-042-2
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Search completed: April 30, 2003, 14:37:38 Job time: 95 secs

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Sequence 11, Appl Sequence 1979; Ap Sequence 4, Appl Sequence 6, Appl Sequence 6, Appl Sequence 1, Appl Sequence 10, Appl Sequence 10, Appl Sequence 110, Appl Sequence 244, Appl Sequence 244, Appl Sequence 204, Appl Sequence 770, Appl Sequence 770, Appl Sequence 770, Appl Sequence 770, Appl Sequence 101, Appl Sequence 101, Appl Sequence 60, Appl Sequence 60, Appl

Sequence 1 Sequence 1 Sequence 1

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1182 GAACGTGGTGCTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGGTCCT 1241
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; Sequence 33159
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq. Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FRASESEQ for Windows Version 3.0
; FLOMER OF SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-770-791-192
US-09-764-853-314
US-09-878-574-15694
US-10-123-155-204
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Pred. No. 2.8e-110;
0; Mismatches 4;
US-10-273-438-9
US-09-774-639-29
US-09-969-709-58
US-10-157-855-16
US-10-223-076-17
US-10-223-076-12
US-10-223-076-12
US-10-223-076-14
US-10-223-076-4
US-10-223-076-4
US-10-223-076-8
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US-09-712-363-101
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           US-09-918-995-33158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4664, Ap
Sequence 3, Appli
                                                                                                                                                                                                                                      (without alignments)
13148.677 Million cell updates/sec
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/cgn2_6/ptodata/1/pubpna/PCT_WWB_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*
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                                   GenCore version 5.1.4\_p5\_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-918-995-33281
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US-09-764-868-279
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 33281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 399
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100.0%; Pred. No. 1.6e-106;
tive 0; Mismatches 0;
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Best Local Similarity 100.
Matches 391; Conservative
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US-09-918-995-33281
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; Bublication No. US20030073623A1
; GENERAL INFORMATION:
    APPLICANT: Hyseq, Inc.
    ITILE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
    TITLE OF INVENTION: ROW VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 3899-01-20
; NUMBER OF SEQ ID NOS: 380344
; SEQ ID NO 33444
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Pred. No. 2.1e-105;
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: 02/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR FILING DATE: 1999-01-20
PRIOR FILING DATE: 1999-01-20
SEQ ID NOS: 38054
SOFTWARE: FASTEREQ for Windows Version 3.0
SEQ ID NO 33355
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99.0%;
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Best Local Similarity 99.09
Matches 389; Conservative
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; ORGANISM: HOMO 8
US-09-918-995-33444
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Score 386;

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TGTCATTGGAGGAAGTATGAACTTCATGATGCATGACCAGCGCACCGGCCCGGCATGGAA 1421
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100.0%; Pred. No. 1.9e-104;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                          GAGTGGTACGCACGCGCACTGCCCTTAC 400
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; OTHER INFORMATION: n = A,T,C or
US-09-918-995-33739
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Best Local Similarity 100.
Matches 384; Conservative
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ORGANISM: Homo sapiens
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Fublication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBT.
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERBNCE: 20411-756
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEX ID NOS: 38054
SEQ ID NO 33843
LENGTH: 401
No. 4.9e-105;
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Pred. No. 6.4e-105;
0; Mismatches 4;
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Best Local Similarity 99.0%;
Matches 388; Conservative (
       98.78;
       Best Local Similarity 98.7
Matches 389; Conservative
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US-09-918-995-33843
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Matches 373; Conserv
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; TYPE: DNA
; ORGANISM: HOMO 8
US-09-918-995-34424
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LENGIH: 408
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                                                   APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20141-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastseQ for Windows Version 3.0
SEQ ID NO 33159
LENGTH: 401
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                                                                                                                                                                                                                                                                                                                                                                                           Score 376.2; DB 9;
Pred. No. 4.1e-102;
0; Mismatches 4;
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SOFTWARE: FastSEQ for Windows Version 3.0
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US-09-918-995-34424
Sequence 34424, Application US/09918995
Publication No. US20030073623A1
 Sequence 33159, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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98.7%;
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OTHER INFORMATION: n
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APPLICANT: Hyseq, Inc.
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Best Local Similarity
Matches 389; Conserv
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LENGTH: 365
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Length 365;
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; Sequence 34099, Application US/09918995
; Sequence 34099, Application US/09918995
; CENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.;
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR PILING DATE: 1999-01-20
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Pred. No. 1.7e-94;
0; Mismatches 19;
  22.3%; Score 350.6; DB 9 98.9%; Pred. No. 1.7e-94; Live 0; Mismatches 4
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SOFTWARE: FastSEQ for Windows Version 3.0
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ilarity 94.9%;
Conservative (
                             Best Local Similarity 98.9
Matches 353; Conservative
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                                                                                     189 TGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCCGGCATGCTGATACTCTTCCT
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                                                                                                                                                                                                                                                                                                            APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED:
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT PAPLICATION NUMBER: US/09/218,095
CURRENT PILING DATE: 1999-01-20
PRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FaatSEQ for Windows Version 3.0
SEQ ID NO 35056
LENGTH: 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 338.2; DB 9;
Pred. No. 8.4e-91;
0; Mismatches 18;
                                                                                                                                         1481 AGGAGTGGTACGCACGCCGCACTGCCCCTTAC 1513
                                                                                                                                                         375 AAGAGTGGGACGCACGGCGCCATGCCCTTAC 407
                                                                                                                                                                                                                            RESULT 10
US_09-918-995-35056
Sequence 35056, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: misc_feature
; LOCATION: (1)...(383)
; CTHER INFORMATION: n = A,T,C or G
US-09-918-995-35056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 95.1%;
Matches 349; Conservative
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ORGANISM: Homo sapiens
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1019 TCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTTTTGCCTTCCTCC 1078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 471;
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: P2021 Nucleic Acids, Proteins, and Antibodies CURRENT APPLICATION NUMBER: US/09/764.853
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 93
LENGTH: 993
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Pred. No. 3.7e-18;
0; Mismatches 125; Indels
                                                                   APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR PRILING DATE: 1999-01-20
NUMBER: OS SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
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Pred. No. 2.4e-31;
0; Mismatches. 12
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Sequence 32388, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
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Patent No. US20020090672A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: n = A,T,C or G
US-09-918-995-32388
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58.7%;
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Best Local Similarity 92.4%;
Matches 146; Conservative
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Best Local Similarity 58.7
Matches 186; Conservative
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; ORGANISM: Homo sapiens
US-09-764-853-79
                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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1139 ACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAACGTGGTGGTCCATG 1198

RESULT 11

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Sequence 14, Application US/10157855 Patent No. US20020170091A1
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58.78;
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956 TCCCTCTGCGAATGTTC 972
                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lassner, Michael
                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 14
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Best Local Similarity
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ORGANISM: Human
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                                                                         US-10-157-855-14
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   AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT
                                                          1199 ACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAG
                                                                                                                                                     600 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT
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APPLICANT: Cases, Sylvaine
APPLICANT: Smith, Steven
TITLE OF INVENTION: Diacylglycerol O-Acyltransferase
FILE REFERENCE: UCAL-105(21P2
CURRENT APPLICATION NUMBER: US/10/273,438
CURRENT FILING DATE: 2002-10-16
PRIOR FILING DATE: 1908-11-09
PRIOR FILING DATE: 1998-11-09
PRIOR APPLICATION NUMBER: PCT/US98/17883
PRIOR PLING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-06-24
PRIOR PLING DATE: 1998-06-24
PRIOR PLING DATE: 1999-06-23
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0; Mismatches 125;
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                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/10273438 Publication No. US20030072757A1
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                                                                                                                                                                                                                                            486 TCCCTCTGCGAATGTTC 470
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36; Conservative
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US-10-273-438-1
                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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Best Local Simi
Matches 186;
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APPLICANT: RUGZINSK, MICHAEL
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyltransferase Related Nucleic
TITLE OF INVENTION: Acyl-CoA:Cholesterol Acyl-CoA:Cholesterol Coursent Fille DATE: 2002-05-31
PRIOR FILLNG DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-05
PRIOR PELICATION NUMBER: 60/088,143
PRIOR FILING DATE: 1998-06-05
PRIOR PELICATION NUMBER: 60/108,389
PRIOR FILING DATE: 1998-11-12
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Patent No. US20020168711A1
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1895;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 95; DB 9; Le
Pred. No. 4.7e-18;
0; Mismatches 125;
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; OTHER INFORMATION: n at position 209 is unknown
US-10-157-855-14
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1079 ATTGCTGGCTCAACGCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGG 1138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            234 AGTGGTGCATCAGACACTTCTACAAGCCCATGCTTCGAC-----GGGGCAGCAGCAAGT 287
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 6.0%; Score 93.8; DB 9; Length 542; Best Local Similarity 58.8%; Pred. No. 6.6e-18; Matches 183; Conservative 0; Mismatches 122; Indels
                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (377)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (397)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (441)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: SITE
LOCATION: (441)
OTHER INFORMATION: n equals a,t,g, or c
LOCATION: (507)
                                                                                                                                                                                                                                                                                                                                                  : LOCATION: (507)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-764-868-587
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                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 587
LENGTH: 542
NUMBER OF SEQ ID NOS: 1510
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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: April 30, 2003, 13:03:20; Search time 1601 Seconds (withments) (#1000 alignments) (#1000 cell updates/sec	red 1569	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Searched: 16154066 segs, 8097743376 residues	Total number of hits satisfying chosen parameters: 32308132 Minimum DB seq length: 0 Maximum DB seq length: 2000000000	ssing: Minim Maxim Listir	r:* em_estba:* em_esthum: em_estin:* em_estmu:* em_estmu:*		13: gp_est1:* 14: gp_est5:* 15: em_estfun:* 16: em_estcon:* 17: gp_est.* 18: em_gss.hum:* 19: em_gss.hum:* 20: em_gss_lnu:* 21: em_gss_lnu:* 21: em_gss_lnu:* 22: em_gss_ln:* 23: em_gss_lnu:* 24: em_gss_lnu:* 25: em_gss_lnu:* 27: em_gss_lnu:* 27: em_gss_lnu:* 27: em_gss_lnu:* 27: em_gss_lnu:* 26: em_gss_lnu:* 27: em_gss_lnu:* 27: em_gss_lnu:*	is the number of results predicted by chance to have eater than or equal to the score of the result being perived by analysis of the total score distribution. SUMMARIES Query	2 335.8 21.4 563 293 298 298 298 298 272.6 17.4 992 298 272.6 17.1 840

source

BASE COUNT ORIGIN

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Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
T=1: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
and -minmatch 12 options.
                                                                                  1 (bases 1 to 563)
Smith T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, L.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett, G.L., Heaton, M.P., Leagreid, W.W., Rohrer, G.A., Chitko-McKown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                               Chordata, Craniata, Vertebrata, Buteleostomi;
Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
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Library made from pooled tissue from day 20 and day
embryos:
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Pred. No. 5.9e-
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Bos taurus"
/db_xref="taxon:9913"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 55 row: 0 column: 15
Seq primer: ATTTAGGTGACACTATAG.
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/lab_host="DH10B"
                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Cetartioda
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85.6%;
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160 c
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AUTHORS
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                                                                                                                                                                                                                                                                                                  3;
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/clone=lib="NCI_CGAP_Li9"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: PCMY-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                            Score 402.4; DB 13; Length 799;
Pred. No. 1.8e-83;
0; Mismatches 126; Indels 16;
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                   /organism="Mus musculus"
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/db_xref="taxon:10090"
                                                                                                                                                                                                                                                              Query Match 25.6%;
Best Local Similarity 78.7%;
Matches 524; Conservative
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                                                                                                                                  BG920709 778 bp mRNA linear EST 05-JUN-2001 602824607F1 NCI_CGAP_Mam6 Mus musculus CDNA clone IMAGE:4953408 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 778)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   976 ATGAGCCGAGAGCCCTTCAGCACCCGTGCCCTGGTGCTCTTATCCTGCATGCCACGTTG 1035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 TACCCAAGGACTCCTACTGTAAGATGGGGTTATGTGTCGCTATGCAGGTTTTACAGGTGTTT 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171 GGCTGCCTGTTTTATGTGTACTACATCTTTGAGAGACTCTGTGCCCCACTATTCCGGAAT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 ATCAAACAGGAGCCCTTCAGTGCTCGTGCCTGTGTGTTTAACTCCATCTTG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       796 CCCAGTTTCTCCCAGCTACCTCTACTTCCTTTCTGCCCAACACTCATCTACAGGGAGACT 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51 CCCACAGTCAACCAGTACCTGTTCCTGTTTGCGCCTACACTTATTTACCGAGACAAC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               856 TACCCTAGGACGCCCTATGTCAGGTGGAATTATGTGGCCCAAGAACTTTGCCCCAGGCCCTG 915
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488 AGGCTGATGATGGANTTCGATCTACTGACCTTCGGCTTCGGACAGCTGCCCTTGGCTCTG 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="Index:4953408"
/clone=lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/lab_host="bH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 298.2; DB 13; Length
Pred. No. 4.2e-59;
0; Mismatches 243; Indels
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19.0%;
Best Local Similarity 65.1%;
Matches 455; Conservative
                             502 GIGACCTGGGTGCCCA 517
                                                         548 GIGACGIGGGICCCCA 563
                                                                                                                                                              mRNA sequence.
BG920709
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// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Homo sapiens"
// Organism="Index Hais | Faranisms |
// Colone="Index Hais | Faranisms |
// Lissue_type="adrenal cortex carcinoma, cell line"
// Index | Index | Index |
// Index | Index | Index |
// Organ: adrenal gland; Vector: pCMV SPORT6; Site_1:
// Not1; Site_2: SalI; Cloned unidirectionally; oligo-dT
primed. Average insert size | 1.23 kb. Library enriched for |
// Full-length clones and constructed by Life Technologies.
// Note: this is a NIH_MGC Library."
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NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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1036 CCAGGCATCTTCATGCTGCTGCTCTTCTTTTGCCTTCCTCCATTGCTGGCTCAACGCC 1095
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CDNA Library Preparation: Life Technologies, Inc.,
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM10161 row: a column: 15
High quality sequence stop: 694.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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1. .705
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BG105735
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Query Match

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/organism="Homo sapiens"/db_xref="taxon:9606"
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Best Local Similarity 63.2%;
Matches 419; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 992)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                     CCTGGGGGTTCTTCTATCCCGTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAA 1382
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                                                                                                                                                                TGTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGTGCCCTGGTGCTCTTATCCT
                                                                                                                                                                                                                     120 CTIGITICGGAATAICAACAGAGCCCTTCAGCGCTCGTGTTCTGGTCCTAIGTGTAIT
                                                                                                                                                                                                                                                                            1 CTACCGTGACAGCTATCCCAGGAATCCCACTGTAAGATGGGGGTTATGTCGCTATGAAGTT
                                                                ;
                                       Length
                                    Score 281.6; DB 12;
Pred. No. 3.1e-55;
0; Mismatches 244;
258
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                                     17.9%;
nilarity 64.2%;
Conservative (
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                                                       Best Local Sim
Matches 439;
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

DEFINITION

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/clone_lib="NCI_CGAP_SKn3"
/clone_lib="NCI_CGAP_SKn3"
/lab_nost="DH10B_TI phage-resistant)"
/iab_nost="DH10B_TI phage-resistant)"
/incte="Organ: skin; vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally, Primer: Oligo dT
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP_Library."
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Email: cgapbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DN
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can if
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
http://image.llh.gov
Right at:
LLAM10593 row. n column: 22
High quality sequence stop: 828.
Location/Qualifiers
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Pred. No. 4.6e-53;
0; Mismatches 244; Indels
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GI:12790932
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AL527439
AL527439.1 GI:127909
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                                                                    BG529751 840 bp mRNA linear EST 03-APR-2001 602560622F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4698748 5',
                                                                                                                                                                            Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (basea 1 to 840)
NIH-MGC http://mgc.noi.nih.gov/.
                                                                                                                                                                                                                                                                                                  CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lnl.gov
Plate: LLCM1529 row: k column: 05
High quality sequence stop: 764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GTGTACTACATCTTTGAAAGGCTTTGTGCCCCCTTGTTTCGGAATATCAAACAGGAGCCC 191
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Pred. No. 5.1e-52;
0; Mismatches 260; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryonal carcinoma"
//lab_host="DH10B (T1 phage-resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                              Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:4698748"
/clone_lib="NIH_MGC_61"
                                                                                                                        BG529751.1 GI:13521288
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Best Local Similarity 63.4%;
Matches 460; Conservative
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                                                                                                mRNA sequence.
BG529751
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                                                                                                                                                      human.
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662 CGT
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL527439 LTI_NFL003_NBC3 Homo sapiens CDNA clone CSODC021XJ22 5
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                            1409 GCCCGGCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAA----TCCAG 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1350 GATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGCGCAC-CG 1408
CIGCTGCTCA-TCTTCTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCCCGAGATGCT 1109
                                                                                                       1110 ACGATTTGGACACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCAACTA 1169
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                              1230 GCTGCGGCTCCTTGGTGCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTTCCTGGTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 893)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
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/lab_host="DH10B"
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/clone="CS0DC021xJ22"
/clone_lib="LTI_NFL003_NBC3"
/sex="male"
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                                                                                                      Gaps
                                                                                                                                                GATGAAGGAAGGCTGGTTGAGTTCAGCCTCCTGTCTTATGCTTTTGGCAAATTTCCT 60
  Medical
  Technologies, a division of Invitrogen 9800 Medical Drive Rockville, Maryland 20850, USA Fax: (1) 301 B371 Email: fliangelifetech.com URL: http://fulllength.invitrogen.com" 8 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         480 TGTCGCYATGAAGTTTGCACAGGTCTTTGGTTGCYTTTTCYATGTGTACCACATCTTTGA
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                                                                              Length 893;
                                                                             Score 264; DB 9; Length 89
Pred. No. 4.5e-51;
6; Mismatches 341; Indels
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Best Local Similarity 58.3%;
Matches 521; Conservative
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 694)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K.; Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3/]; double stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTyT3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo.
     EST 16-MAR-1998
AA867129 cv23f11.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1265325 5' similar to gb:L42293 Mus musculus acyl-coenzyme A:cholesterol acyltransferase (MOUSE);, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; contact the IMAGE consortium (info@image.llnl.gov) for further information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1056 GCTCATCTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCCCGAGATGCTACGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="InAGE:1265255"
/clone=lib="Soares_thymus_2NbMT"
/sex="male"
/tissue_type="Thymus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
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Pred. No. 5.9e-47;
0; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                              The WashU-HHMI Mouse EST Project
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High quality sequence stop: 441.
Location/Qualifiers
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/lab_host="DH10B"
                                                                                                                          AA867129.1 GI:2962574
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Local Similarity 63.4%;
Les 377; Conservative
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TTGCCCAGGCCCTGGGATGTGTGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:802563"
/clone_lib="NOI_CGAP_Skn3"
/lab_most="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                              1236 GCTCCTTGGTGCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTGTTCCTGGTCTCCGCAGT 1295
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Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLANLOGOF row: pc. column: 20
High quality sequence start: 5
High quality sequence stop: 738.
182 TGGTGACAGGATGTTTTATAAGGACTGGTGGAACTCTACATCATACTCCAACTACTACAC 241
                                                                242 GACCTGGAACGTGGTGCACGACTGGCTCTACTACTATTTACAAAGACCTGCTCTG 301
                                                                                                                                                 361
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1 (bases 1 to 741)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                               482 CTCGAACATCACGGTTTGGGCTTCTCTGTTCCTGGGCTATGGACTCATTCTGTGCTTTTA 541
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                                                                                                                                                 GTTTTTCTCGAAGAGGTTCAAATCTGCCGCCATGCTGGCCGTCTTCGCCCTGTCGCTGT
                                                                                                                                                                                                                                                                                                                                                                                CTGCCAGGAGTGGTACGCACGGCGCACTGCCCCTTACCCCAGGCAACTTTCTGG 1530
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llarity 63.9%; Pred. No. 1.2e-46;
Conservative 0; Mismatches 225; Indels
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BG696168
BG696168.1 GI:13961039
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Best Local S
Matches 402
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BG696168
LOCUS
DEFINITION
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VERSION
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TITLE
JOURNAL
COMMENT
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ub37ell.rl Soares_thymus_2NbMT Mus musculus cDNA clone IMAGE:1379948 5' similar to 9b:L21934 STEROL O-ACYLTRANSFERASE (HUMAN); 9b:L42293 Mus musculus acyl-coenzyme A:cholesterol acyltransferase (MOUSE);, mRNA sequence.
AI049480.1 GI:3297767
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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961
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Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                            132 TTAACTCCATCTTGCCAGGTGTGCTGATTCTCTTCCTTACTTTTTTTGCCTT-TTGCACT
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WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
WashIngton Park Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
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                                                                                                                                                                                                                                                                                                                                                                                                                             3/]; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:902416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GETGCACGAGTATGCCCTCGCCATCTGCCTGAGTTACTTCTACCGGGTGCTCTTCGTGCT 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    490 TCCTGGACATCATGGTTTGGGCTTCTCTGTTCCTGGGCTATGGACTCATCCTGTGCTTTT
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Pred. No. 7.2e-46;
0; Mismatches 214;
                                                                                                                                                                                                                                                                /clone_lib="Soares_thymus_2NbMT"
                                                                                                           Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                             High quality sequence stop: 313.
Location/Qualifiers
                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:1379948"
                                                                                                                                                                                                                                                                                                    /tissue_type="Thymus"
                                                                                                                                                                                                        /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 15.4%;
Local Similarity 63.9%;
nes 381; Conservative
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846 bp mRNA linear EST 27-MAR-2001 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4669480 5',
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Department of Virology
Institute of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
Brail: Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Bmail: ysuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano
S. Construction and characterization of a full length-enriched and
a 5'-end-enriched CDNA library. Gene 200 (1-2), 149-156 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suzuki,Y., Tsunoda,T., Taira,H., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Nakamura,Y., Morishita,S., Okubo,K., Suyama,A. and Sugano,S.
In silico mapping of the 5'-ends of human mRNAs using full-length enriched and 5'-end enriched cDNA libraries constructed by
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                                                                                                                                     05-APR-2001
                                                                                                                                     AU099137 AU099137 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HEP20912 similar to Homo sapiens acyl coenzyme A:cholesterol
                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Sugano Homo sapiens cDNA library"
/note="Differential display comparison of untreated and
dimethylfumarate treated U937 cells"
79 c 108 g 35 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TGGACCCGACACATGGAGGCTGTGAAGGCACAATTGCTGGAGCAAGCGCAGGGACAACTG
550 ATTCTCAAGAGTGGTATGCCCGCCAGCACTGTCCTCTGAAGAACCTACATTTCTGG 605
                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelk
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 300)
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Pred. No. 1.1e-45;
); Mismatches 0;
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100.0%; Pred. No. 1...
... 0; Mismatches
                                                                                                                                                                                                          acyltransferase 2 mRNA, mRNA sequence. AU099137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="HEP20912"
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                                                                                                                                                                                                                                                                           AU099137.1 GI:13550266
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Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.3°
Best Local Similarity 100°.
Matches 240; Conservative
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BG500675.1 GI:
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AA867128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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KEYWORDS
SOURCE
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                                                                                                   Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nh.gov
Tissue Procurement: DCTD/DTD

Tobna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llni.gov
Plate: LLCM1481 row: g column: 17

High quality sequence stop: 684.
                 Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCAA 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    988 CCCTTCAGCACCCGTGCCCTGGTGCTCTCTATCCTG-CATGCCACGTTGCCAGGCATCTT 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1047 CATGCTGCTCCTCTTTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCCGAGAT 1106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  253 GATTCTCTTCCTTACTTTTTTGCCTTTTTGCACTGCTGGCTCAATGCCTTTGCTGAGAT 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                811 TACGTCTACTTCCTCTTCTGCCCAACACTCATCTACAGGGAGACTTACCCTAGGACGCCC 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           871 TATGT-CAGGTGGAATTATGTGGCCAAGAACTTTGCCCAGGCCCT--GGGATGTGTGTGCTC 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73 ACTGTGAAGATGGGGTTATGTTGCTATGAACGTTTGCACAGGTCTTCTGGTTGCTTTTTC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        928 TATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTTTGCCAACATGAGCCGAGAG 987
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                                            1 (bases 1 to buy)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                              Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 247;
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                Chordata; Craniata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.2%; Score 238.8; 63.2%; Pred. No. 3.5
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4669480"
              Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 846)
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EST 16-MAR-1998
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Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptce,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                               1287 CTCCGCAGTGGCCCATGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCCGTCAT 1346
                                                                                                                                                                                                                                                                                              1406 CCGCCCCGCCATGGAACGTGCTGATGTGGACCATGCTGTTTCTAGGCCAGGGAATCCAGG 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nacovize 887 bp mRNA linear EST 16-MAR-vx23f10.rl Scares thymus_2NbMT Mus musculus cDNA clone IMAGE:1265323 5' similar to qb:L21934 STEROL O-ACYLTRANSFERASE (HUMAN); qb:L42293 Mus musculus acyl-cenzyme A:cholesterol acyltransferase (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
1227 TGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAGGGGTAGCCATGCTGGTGTTGCTGGT 1286
                                                                                                                                                                                               1347 GCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAGC-GCA 1405
                                                                                                                                                                                                                                                612
                                                                                                                                                                                                                                                                                                                           MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Soares_thymus_2NbMT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: -28ml3 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
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The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 447.
Location/Qualifiers
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/clone="IMAGE:1265323"
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
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                                                                                                                                           1064
                                                                                                                                                                                                                                                                                                            CGTGGTGGTCCATGACTGGCTGTACAGCTACGTGTATCAGGATGGGCTGCGGCTCCTTGG 1244
                                                                                                                                                                                                                                                                                                                                                                                                                          GTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCCGTCATGCTGATACTCTTCCTTGT 1364
                                                                                                                                                                                                 CTTTGCCTTCCTCCATTGCTGGCTCAACGCCTTTGCCGAGATGCTACGATTTGGAGACAG 1124
                                                                                                                                                                                                                                                      1125 GATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTCTCCAACTACTACCGCACTTGGAA 1184
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                                                                                                                                                                                                                242 GAAGAGGTTCAAATCTGCCGCCATGCTGGACGTCTTCGCCCTGTCGGCTGTGGTGCACGA
                                                                                                                                             1005 CCTGGTGCTCTATCCTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTT
                                                                                                                                                                2 CCTGGTCCTGTGTGTTTAACTCCATCTTGCCAGGTGTCTTGATACTGTTTCGTT
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BAC end sequences of Library PTB
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fullyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
  Library went th
constructed by
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Pan troglodytes DNA, clone: PTB-145020.F,
AG133295
provided by Dr. Bertrand Jordan. rounds of normalization, and was Soares and M.Fatima Bonaldo."
                                                                                    Score 233.8; DB 9;
Pred. No. 5.2e-44;
0; Mismatches 197;
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64.1%;
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                                                                                                                  Matches 352;
                                                                                         Query Match
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BG697784 1inear EST 07-MAY-2001
602661272F1 NCI_CGAP_SKn3 Homo sapiens CDNA clone IMAGE:4804481 5',
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and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 848)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 GIGACCIGGGIGCCCAIGTITTCIGICCACCCIGITGGCGCCGIACCAGCCCTGCGGAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442 AGGCTGCTGCTGCAGTTTGACCTACTGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 227.6; DB 17;
Pred. No. 1.3e-42;
); Mismatches 14; I
                                                                                                                                                                                                                                                                                                          1. 635
/organism="Pan troglodytes"
/db_xref="taxon:9598"
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                                                                                                                                                                                                                                                                                                                                                                                        //sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee
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BG697784
BG697784.1 GI:13964385
                                                                                                                                                                              Sequencing: -21M13
                                                                                                                                      clone tracking errors.
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90.6%;
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Best Local Similarity 90.6
Matches 259; Conservative
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R.Site 1
R.Site 2
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                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9506"
/db_xref="taxon:9506"
/clone=lib="kci.4804481"
/clone=lib="kci.GcAP_Skn3"
/lab_host="bH10B (Tl phage-resistant)"
/note="Organ: skin; Vector: pcWV-SPORT6; Site_1: NotI;
Site_2: Sali; cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

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                                                                                                                                                                                                                                                                                                 Score 222.4; DB 12;
Pred. No. 2.4e-41;
0; Mismatches 196;
http://image.llnl.gov
Plate: LLAM10701 row: p column: 18
High quality sequence stop: 808.
Location/Qualiflers
1..848
                                                                                                                                                                                                                                                                                                   14.2%;
63.4%;
                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.4 Matches 340; Conservative
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15792.059 Million cell updates/sec
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1 atggagccagggggcccg.........ttggtcctgccatacctag 1569
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	-3 Sequence 3, Appli	A-3 Sequence 3, Appl	Sequence 4,			-5649 Sequence 5649,	S	A-1 Sequence 1, Appl			-10898 Sequence 10898, 1	S		-2800 Sequence 2800,	-109 Sequence 109, App	-109 Seguence 109, App	Sequence 6552	Sequence	-4846 Sequence 4846, Ap	-10353 Sequence 10353	-9964 Sequence 9964,
ID	PCT-US02-22746-3	US-09-918-026A-3	US-09-630-892-4	US-09-630-892A-4	US-09-328-857	US-60-360-207-5649	PCT-US02-22746-10	US-09-328-857A-1	US-09-918-026A-10	US-60-229-512-505	US-60-360-207-10898	PCT-US02-18947	US-10-172-118-388	US-09-770-173-2800	PCT-US02-21664-109	US-10-191-997-109	US-09-474-436-6552	US-08-657-621A-1	US-09-606-776-4846	US-09-644-873-10353	US-09-652-126-9964
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Query	100.0	100.0	99.7	99.7	6.06	71.0	70.9	70.9	70.9	34.7	26.9	26.0	26.0	25.9	25.9	25.9	25.9	25.9	25.9	25.9	25.9
Score	1569	1569	1564.2	1564.2	1425.8	1113.4	1112.4	1112.4	1112.4	544.8	421.4	407.2	407.2	405.6	405.6	405.6	405.6	405.6	405.6	405.6	405.6
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8 25 US-09-652-355-11001 Sequence 11001, A Sequence 10023, A Sequence 10027, A Sequence 1027, A Sequence 10	ALIGNMENTS TUS0222746 Licals, Inc. ooke amonidis STECTUS0222746 SSION 09/918,026 7-30	E: E: Ex: CDS ON: (1)(1569) 2746-3 LOD.0%; Score 1569; DB 1; Length 1569; al Similarity 100.0%; Pred. No. 0; 1569; Conservative 0; Mismatches 0; Indels 0; Gaps ATGGAGCCAGGCGGGCCCTTGCAGAGGACAGAGGGTGGGAGGGG 60 ATGGAGCCAGCCGGTCTGCAGAGGACAGAGGCTGGGAGGGG 60 ATGGAGCCAACCTGTGAAGAACATGAGAAGAAGGCTGGGAGGGG 60 GAGGCCAACCTGTGAAGAACATGAGAAAGAAGGCTGGAGGGGGGGG
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APPLICANT: Sturley, Stephen L
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                                                                                                                  APPLICANT: Sturley, Stephen L.
APPLICANT: Oelkers, Peter
TITLE OF INVENTION: ISOLATION OF A GENE
TITLE OF INVENTION: ACYLTRANSFERASE
FILE REPRENENCE: 0575/56331-A
CURRENT APPLICATION NUMBER: US/09/630,892
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 32
SOSTWARE: Patentin Ver. 2.0
SEQ ID NO 4
                                                                                                  Sequence 4, Application US/09630892
GENERAL INFORMATION:
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Best Local Similarity 99.83
Matches 1566; Conservative
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                                        CATACCTAG 1569
                                                                                                                                                                                                       ; LENGTH: 2040
; TYPE: DNA
; ORGANISM: Yeast
US-09-630-892-4
                                                 CATACCTAG
                                                                                    RESULT 3
US-09-630-892-4
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                        ATCTACAGGGAGACTTACCCTAGGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAAC
                                                                 TTTGCCCAGGCCCTGGGATGTGTGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTT
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APPLICANT: Novak, Sabine
APPLICANT: Brickson, Sandra
APPLICANT: Erickson, Sandra
TITLE OF INVENTION: Novel Acyl CoA.Cholesterol Acyl
TITLE DF INVENTION: Transferase (ACAT-2)
ETLE REFERENCE: 6510-1044US1
CURRENT APPLICATION NUMBER: US/09/328,857A
CURRENT FILING DATE: 1999-06-08
PRION FILLING DATE: 1998-06-23
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GENERAL INFORMATION:
'APPLICANT: Cases, Sylvaine
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LECULATION OF A GENE ENCODING DIACYLGLYCEROL ACYLTRANSFERASE
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Pred. No. 0;
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                           FILE REFERENCE: 0575/56311-A
CURRENT APPLICATION NUMBER: US/09/630,892A
CURRENT FILING DATE: 2000-08-02
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 2040
                                                                                                                                                    99.7%;
Similarity 99.8%;
6; Conservative
         TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                      ORGANISM: yeast
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Matches 1566;
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TYPE: DNA

CRGANISM: human

FEATURE:

NAME/KEY: misc_feature

CAGATION: (571)...(571)

OTHER INFORMATION: N is a,

NAME/KEY: misc_feature

CAGATION: (573)

OTHER INFORMATION: N is a,

US-09-328-857A-2.
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APPLICANT: ROSABINE M. CROOKE
APPLICANT: Mark J. Graham
APPLICANT: Mark J. Graham
APPLICANT: Mark J. Graham
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
TITLE OF INVENTION: EXPRESSION
FILE REFERENCE: ISPH-0694
CURRENT APPLICATION NUMBER: PCT/US02/22746
PRIOR APPLICATION NUMBER: 09/918,026
PRIOR APPLICATION NUMBER: 09/918,026
NUMBER OF SEQ ID NOS: 65
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Pred. No. 1.4e-237;
0; Mismatches 247;
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LOCATION: (30)...(1607)
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Pred. No. 1.4e-237;
0; Mismatches 247; Indels
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APPLICANT: Cases, Robert
APPLICANT: Cases, Robert
APPLICANT: Brickson, Sabine
TITLE OF INVENTION: Novel Acyl CoA.Cholesterol Acyl
TITLE OF INVENTION: Transferase (ACAT-2)
TITLE OF INVENTION: Transferase (ACAT-2)
FILE REFERENCE: 6510-104051
CURRENT APPLICATION NUMBER: US/09/328,857A
CURRENT FILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: 60/090,354
PRIOR APPLICATION NUMBER: 60/090,354
NUMBER OF SEQ ID NOS: 8
SOFURMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (176)...(176)
OTHER INCRATION: N means a, g, c or
US-09-328-857A-1
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APPLICANT: Cases, Sylvaine
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Best Local Similarity 83.2%;
Matches 1295; Conservative
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ORGANISM: mouse
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US-09-328-857A-1
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APPLICANT: Rosannew. Crooke
APPLICANT: Mark J. Graham
APPLICANT: Kristina M. Lemonidis
TITLE OF INVENTION: ANTISENSE MODULATION OF ACT
FILE REFERENCE: ISPH-0588
CURRENT APPLICATION NUMBER: US/09/918,026A
CURRENT FILING DATE: 2001-07-30
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                   Score 1112.4;
Pred. No. 1.4e-
0; Mismatches
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8-09-918-026A-10
Sequence 10, Application US/09918026A
GENERAL INFORMATION:
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NAME/KEY: unsure
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US-09-918-026A-10
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Matches 1295; Conser
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NUCLEIC ACID MOLECULES ENCODING SE II PROTEINS, AND USES THEREOF 5 1200 1260 1320 1020 1080 848 728 809 960 899 900 GCTGGATCGGGCCATGCGGGAGGCTATACAATCCTACCCATCACAAGACAAACCTCTGCC 248 CATCTTGCCCGGTTGTGAACTCAGTCCTCTTGGCTGACTGTGCCCAACACTCATCTACAG GGCCCTGGGATGTGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTCCTGTCTT TTTAGCCGCCCACGCCGTGGTGCTCTGCGCGCTGCCGGTCCACGTGGCCGTGGAGCATCA 1081 ACGGACAGGAAGGAACCAGCIGGIGCCGATCCTTCGTGCCAGACGAGGTGAGGCTT CCAGGCCCCCAGTTTCTCCAGCTACCTCTACTTCCTCTTCTGCCCAACACTCATCTACAG GGAGACTTACCCTAGGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAACTTTGCCCA 781 CATTGATGAGGCCAGGTAGGTCCCCTTCCCACCTGGGACAGGCACACCTATCTGATCAGA 961 GCTAGCGCCCACGCCGTGGTGCTCTGCGCGCTGCCGGTCCACGTGGAGCATCA GCTCCCGCCGGCCTCCCGGTTGTCTCGTCTTCGAGCAGGTTAGGTTCCTGATGAAAAG CTACTCCTTCCTGAGAGGCTGTGCCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGAT TTTCATCATCGCAAGTCCCTGCTTGATGAGCTGATGGAGGTGCAGCATTTCCGCACCAT GTAGCAAGGATCATGAGCCCTGCTTGAGTAAGTCGGGGTGATGACAAGTAATGGGAGGAA CTACCACATGTTCATCGCTGGCCTGTGTCTTCATCATCAGCACCCTGGCCATCGACTT CATTGATGAGGCCAGGCTGCTGCTGGAGTTTGACCTACTGATCTTCAGCTTCGGACAGCT PHASE II PROTEINS, AND CCCACCTCCCCCAGGTTCCTTGAGCAGGACCCAGGAGCCATCCCTGGGGAAACAGAAAĠT Length 2154; Indels Sequence 505, Application US/60229512
GENERAL INFORMATION:
APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PHASE II
TITLE OF INVENTION: BRUG-METABOLIZING PROTEINS, NUC
TITLE OF INVENTION: HUMAN DRUG-METABOLIZING PHASE
FILE REFERENCE: CL000770
CURRENT APPLICATION NUMBER: US/60/229,512
CURRENT FILING DATE: 2000-095
NUMBER OF SEQ ID NOS: 516 99 Score 544.8; DB 66; Pred. No. 6.3e-111; 0; Mismatches 357; FEQ ID NOS: 516 FastSEQ for Windows Version 4.0 34.7%; 65.8%; Query Match
Best Local Similarity 65.8
Matches 878; Conservative TYPE: DNA
CRGANISM: HUMAN
US-60-229-512-505 SEQ ID NO 505 SOFTWARE: LENGTH: 1021 1261 1141 849 1201 609 729 789 606 a ŏ

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  TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGT
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                       TGGCCTATGCTTTTGGCAAATTTCCTACTGTTATTTGGACATGGTGGGCCATGTTCCTGT
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                                               CCACCCTGTTGGCGCCGTACCAGGCCCTACGGCTGTGGGCCAGGGG-
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                                              CACGTTGCCAGGTGAGCCAACTAAGGTAGGCTAGAGCAGCTGTGCCCTGGGGAAGGCTA
                                                                                           CAACGCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAA
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 TGCCAACATGAGCCGAGAGCCCTTCAGCACCCGTGCCCTGGTGCTCTCTATCCTGCATGC
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Pred. No. 2.3e-83;
0; Mismatches 506;
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US-60-360-207-10898
Sequence 10898, Application US/60360207
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUANN GENOME DISCOVERY SYS
FILLE REFERENCE: CL001321
CURRENT APPLICATION NUMBER: US/60/360,207
CURRENT FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 10898
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59.2%;
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US-60-360-207-10898
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Best Local Si
Matches 769;
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L21934
DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-388
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ORGANISM: HOMO
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APPLICANT:
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                                                                                            Sequence 388, Application PC/TUS0218947
Sequence 388, Application PC/TUS0218947
APPLICANT: Rosetta Inpharmatics
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-175-228
CURRENT APPLICATION NUMBER: PCT/US02/18947
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 388
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              Score 407.2; DB 1;
Pred. No. 3.6e-80;
0; Mismatches 508;
CTTTCTGGGGGCTGGTGACACCTCGATCTTGGTCCTGCC 1561
                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: L21934
DATABASE ENTRY DATE: 2001-06-18
PCT-US02-18947-388
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Best Local Similarity 59.0%;
Matches 768; Conservative (
                                                                                            PCT-US02-18947-388
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GAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGTGGAACTCAACGTCCTTC 1161
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APPLICANT: Bernards, Rene
APPLICANT: Bernards, Rene
APPLICANT: Bernards, Rene
FILLE REFERENCE: 9301-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CURRENT FILLING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
SEQ ID NO 388
SEQ ID NO 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 388, Application US/10172118; GENERAL INFORMATION:
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Van de Vijver, Marc
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Roberts, Chris
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                                                        ATCTTCATGCTGCTCATCTTCTTTGCTTCCTCCATTGCTGGCTCAACGCCTTTGCC 1101
                                                                                                       AAGTGGACCACATCAGAACAATATATCACATGTTTATTGCCCTCCTCATTCTCTTTATCC 1856
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                                                                                   AGGTGCAGCATTTCCGCACCATCTACCACATGTTCATCGCTGGCCTGTGTGTCTTCATCA 406
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    Length 4011;
   DB 41;
                        0; Mismatches 508;
Score 407.2; DB 4
Pred. No. 3.6e-80;
  26.0%;
59.0%;
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  GCTGTATCTGCTGTAGTACACGAATATGCCTTGGCTGTTTGCTTGAGCTTTTTCTATCCC
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GENERAL INFORMATION:
APPLICANT: White, David
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL NUCLEIC ACID MOLECULES AND USES
TITLE OF INVENTION: THEREPOR
FILE REFRENCE: 1600.2059-001
CURRENT APPLICATION NUMBER: US/09/770,173
CURRENT FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-28
NUMBER OF SEQ ID NOS: 3167
SOUTHWARE: FEASTSEQ for Windows Version 4.0
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US-09-770-173-2800
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GENERAL INFORMATION:
APPLICANT: Oligos Etc., Inc.
APPLICANT: ARROW, Amy
APPLICANT: THOMPSON, Terry
TITLE OF INVENTION: Their Use
FILE REFERENCE: 54800-5019WO
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58.9%; Pred. No. 7.6e-80;
11ve 0; Mismatches 509;
                                                                                                                                                                                                                  , NAME/KEY: misc_feature
, OTHER INFORMATION: ACAT-1: Acc. No. XM_031119
PCT-US02-21664-109
APPLICATION NUMBER: PCT/US02/21664
CURRENT APPLICATION NUMBER: PCT
CURRENT FILING DATE: 2002-07-1
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2001_07-10
                                                                       NUMBER OF SEQ ID NOS: 132
SOFWARE: Patentin version 3.1
SEQ ID NO 109
LENGTH: 2729
                                                                                                                                                                                                                                                                                                                         Best Local Similarity 58.9
Matches 767; Conservative
                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                             TYPE: DNA
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1263 GTGCTGATTCTCTTCCTTACTTTTTTGCCTTTTTGCACTGCTGGCTCAATGCCTTTGCT 1322
                                                                                                                               1222 CAGGATGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAGGGGTAGCCATGCTGGGTGTTC 1281
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                                                                            1162 TCCAACTACTACCGCACTTGGAACGTGGTGCTCCATGACTGGCTGTACAGCTACGTGTAT 1221
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Run on:

Sequence:

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APPLICANT: CARCILL, Michele
APPLICANT: CRUDE, Andrew
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALMEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116233
SOFTWARE: FASTESEQ for Windows Version 4.0
                                                     Sequence 82168, A
Sequence 82169, A
Sequence 82160, A
Sequence 82166, A
Sequence 82166, A
Sequence 82160, A
Sequence 82160, A
Sequence 82160, A
Sequence 82161, A
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1 US-60-453-135-82165

1 US-60-453-135-82166

1 US-60-453-135-82168

1 US-60-453-135-82170

1 US-60-453-050-82165

1 US-60-453-050-82166

1 US-60-453-050-82168

1 US-60-453-050-82169

1 US-60-453-050-82169

1 US-60-453-050-82164

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1 US-60-453-050-82164

1 US-60-453-135-82167

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1 US-60-453-158-15147

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1 US-60-453-3158-13167

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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 12201, Application US/60452680 GENERAL INFORMATION:
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Best Local Similarity 99.6%;
Matches 1562; Conservative
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122.88
122.112.22.88
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                                                                                                                                                                                                                (without alignments)
13964.161 Million cell updates/sec
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2. /cgn2_6/ptodata/1/pna/USO6_NEW_COMB.seq:*
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                             GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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1 US-10-144-771-16998

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Minimum DB Maximum DB

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QQ	301	CAGAAAGITITCATCATCCGCAAGICCCTGCTTGATGAGCTGATGGAGGTGCAGCAITTC 360	
٥٧ مو	361	CGCACCATCTACCACATGTTCATCGCTGGCCTGTGTGTCTTCATCATCAGCACCCTGGCC 420	
Oy Db	21	TCGACTTCATTGATGAGGGAGGCTGCTGCTGGAGTT TCGACTTCATTGATGAGGGCAGGCTGCTGCTGGAGTT TCGACTTCATTGATGAGGGCAGGCTGCTGCTGGAGTT	
Qy Db	⊣ ⊣	SCCATTGGCGCTGGTGACCTG 	
Oy Db	541	CCGTACCAGGCCCTACGGCTGTGGGCCAGGGGCACCTGGACGCGACGGGCCTGGGC 600	
Qy	601	TGTGCGCTTTTAGCCGCCCAGCCGTGGTGCTCTGCGCGCTGCCGGTCCACGTGGCCGTG 660	
Oy Dp	661	GAGCATCAGCTCCCGCCGGCTCCCGTTGTGTCCTGGTCTTCGAGCAGGTTAGGTTCCTG 720	
Oy Db	721	ATGAAAACTACTCCTGAGAGAGGCTGTGCCTGGGATCCTTCGTGCCAGACGAGGT 780	
Qy	781		
Qy	841	racagggagáci 	
Oy Db	901	TITGCCCAGGCCCTGGGATGTGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTT 960	
Qy Db	961 961	CCTGTCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCCGTGCCCTGGTGCTCTCTATC 1020	
o o	1021	CIGCAIGCCACGITGCCAGGCAICTICAIGCIGCIGCICAICTICITIGCCITCCCAI 1080	
Qy	1081	TGCTGGCTCAACGCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGAC 1140 	
Qy	1141	TGGTGGAACTCAACGTCCTTCTCCAACTACTGCACCTTGGAACGTGGTGGTCGTCCATGAC 1200 	
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US-60-453-135-7616
US-60-453-135-7616
Sequence 7616, Application US/60453135
Sequence 7616, Application US/60453135
Sequence 7616, Application US/60453135
Sequence 7616, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, MICHELE
TITLE OF INVENTION: MYCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WINBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
CURRENT FILING DATE: 2003-03-10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7616
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241 CCTCTGCCCCCAGCTCCCCAGGTTCCTTGAGCAGGACCAGGAGCATCCCTGGGGAAA 300
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99.8%; Score 1566.2;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1562; Conservative 7; Mismatches
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ORGANISM: Homo sapiens
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                                                                                          Score 1564.2;
Pred. No. 0;
0; Mismatches
                           4.0
                   207012
Windows Version
                                                                                           99.78;
          2000-09-08
PRIOR APPLICATION NUMBER: 6(
PRIOR FILING DATE: 2000-09-(
NUMBER OF SEQ ID NOS: 20701:
SOFTWARE: FastSEQ for Windov
SEQ ID NO 5159
LENGTH: 1569
                                                                                                               Conservative
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                                                        ; TYPE: DNA
; ORGANISM: Huma:
US-09-949-016-5159
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OF DETECTION AND
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASS.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF
FILE REPERENCE: CLOOU307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PILING DATE: 2000-10-20
PRIOR PAPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
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1141 TGGTGGAACTCCAACGTCCTTCTCCAACTACTACCACTTGGAACGTGGTGGTCCATGAC 1200 	6	CAGAAAGTTTTCATCATCCGCAAGTTCCTTGAGCAGGCCCAGGAGCCCATCCTGGGGAAA CAGAAAGTTTTCATCATCCGCAAGTCCCTGCTTGATGAGCTGATGGAGGTGCAGCATTTC
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1261 GTAGCCATGCTGGTGTTCCTGGTCTCCGCAGTGGCCCATGAGTATCTTCTGCTTC 1320 	g & g	21 ATCGACTTCATTGATGAGGGCAGGCTGCTGCTGTGTGTGT
1321 GTCCTGGGGTTCTTCTATCCCGTCATGCTGATACTCTTGTCATTGGAGGAATGTTG 1380	g & g	1 STOCKTITCHITCHITCH CONTROLL
1381 AACTICATGATGCATGACCAGCGCCCGGCATGGAACGTGCTGATGTGGACCATG 1440	3 6 8	41 CGTACCAGGCCTACGGCTGTGGGCCAGGGCACCTGGACGAGGCGACGGGCCTGGGC
1441 CTGTTTCTAGGCCAGGGAATCCAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGG 1500	8 % E	TGTGCGCTTTTAGCCGCCCACGCGTGCTCTGCGCGCTGCCGGTCCACGTGCCGTG
1501 CACTGCCCTTACCCCAGGCAACTTTCTGGGGGCTGGTGACACCTCGATCTTGGTCCTGC 1560	3 & g	GAGCATCAGCTCCCGCCGCCTCCCGTTGTGTCCTCGTCTTCGAGCAGCAGTTAGGTTCCTG GAGCATCACCTCCCGCCGCCCCCCTCCCGTTTTGTTTCGTCTTCGAGCAGCATTAGGTTTCTG GAGCATCACCTCCCGCCGCCCCCCCTTGTTGTTCTTCGAGCAGGTTAGGTTCCTC GAGCATCACCTCCCGCCGCCCCCCTTGTTGTCTCTTGTTTTTTTT
1561 CATACCTAG 1569 1 1561 CATACCTAG 1569	Qy Db	ATGAAAAGCTACTTCCTTCAGAGAGAGCTGTGCCTGGGATCCTTCGTGCCAGACGAGGT 7
SULT 5 -10-170-235-23912 Sequence 23912, Application US/10170235	Qy Dp	781 GAGGGGATCCAGGCCCCCAGTTTCTCCAGCTACCTCTACTTCCTCTTCTGCCCAACACTC 840
ENERAL INFORMATION: TITLE OF INVENTION: KITS, SUCH AS NUCLEIC ACID ARRAYS, COMPRISING A MAJORITY OF HUMAN TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF	Qy	841 ATCTACAGGGAGACTTACCCTAGGACGCCCTATGTCAGGTGGAATTATGTGGCCAAGAAC 900
CURRENT APPLICATION NUMBER: US/10/170,235 CURRENT FILING DATE: 2003-03-17 NUMBER OF SEQ ID NOS: 42514	Qy	901 TTTGCCCAGGCCTGGGATGTGGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTT 960
LENGTH: 1983 TYPE: DNA OGGANLEN: HUMAN	ζο GO	961 CCTGTCTTGCCAACATGAGCCGAGAGCCCTTCAGCACCGTGCCCTGGTGCTCTCTATC 1020
99.7%; Score 1564.2; DB 8; Length 1983; nilarity 99.8%; Pred. No. 0;	Qy Dp	1021 CTGCATGCCACGTTGCCAGGCATCTTCATGCTGCTCCTCATCTTTGCTTCCTCCCT 1080
Matches 1905; Conservative U; Mismatches 3; Indels U; Gaps U; 1 ATGGAGCCAGGCGCGCCTCTGCAGAGGACAGAAGGCTGGGAGGGGAGCGG 60	Qy	1081 TGCTGGCTCAACGCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGC 1140

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                                                                                                                                                                                                                                                                                                                                              Score 1113.4; DB 9;
Pred. No. 3.4e-255;
); Mismatches 246;
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TITLE OF INVENTION: HUMAN GENOME DISCOVERY
FILE REFERENCE: CLOO1321
CURRENT APPLICATION NUMBER: US/10/144,771
CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 5649
LENGTH: 1607
                                                                                                                                                                                                                                                Sequence 5649, Application US/10144771 GENERAL INFORMATION:
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illarity 83.2%;
Conservative 0
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US-10-144-771-5649
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Matches 1296;
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Sequence 388, Application US/10342887
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APPLICANT: He, Yudong
APPLICANT: Linsley, Peter S.
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: HUMAN GENOME DISCOVERY SYSTEM AND USES THEREOF
FILE REFERENCE: CL001321
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Pred. No. 3.4e-90;
0; Mismatches 506;
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CURRENT FILING DATE: 2002-05-15
NUMBER OF SEQ ID NOS: 47235
SEQ ID NO 10898
LENGTH: 2924
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ilarity 59.2%;
Conservative
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Best Local Similarity
Matches 769; Conserv
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; ORGANISM: HUMAN
US-10-144-771-10898
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APPLICANT: Linsley, Peter S.
APPLICANT: Roberts, Christopher J.
APPLICANT: Roberts, Christopher J.
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van de Vijver, Marc J.
APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Bre
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: 06/298,918
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
PRIOR FILING DATE: 2002-06-14
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SPRIOR FILING DATE: 2002-06-14
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                                                                  26;
                                                4011;
                                                 Length
                                                                   Indels
                                               Score 407.2; DB 9;
Pred. No. 9.2e-87;
0; Mismatches 508;
                                                26.0%;
59.0%;
                                                         Best Local Similarity 59.0 Matches 768; Conservative
          TYPE: DNA
CORGANISM: Homo sapiens
US-10-342-887-388
  LENGTH: 4011
                                                   Query Match
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Sequence 313, Application US/60440068
GENERAL INFORMATION:
APPLICANT: NALER: STEVEN G.
APPLICANT: CARMAN, JULIE
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE
TITLE OF INVENTION: NF KB PATHWAY
FILE REFERENCE: 3053-4191
CURRENT APPLICATION NUMBER: US/60/440,068
CURRENT FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PATENTIN OF 2.1
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                                                                                                                       CAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGGCACTGCCCCTTACCCCAGGCA
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                                           AAGGACTITCTCTGGTTTTTCTCCAAGAGATTCAAATCTGCTGCCATGTTAGCTGTCTTT
                                                                                                                                                                                                                              2816 GIGCICITCGIGCICITCAIGITCITIGGAAIGGCITICAACTICAIIGICAAIGAIAGI
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                                                                                          CTGGTCTCCGCAGTGCCCCATGAGTATATCTTCTGCTTCGTCCTGGGGGTTCTTCTATCCC
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Best Local Similarity 59.0%;
Matches 768; Conservative
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US-60-440-068-313
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SEQ ID NO 313
LENGTH: 4011
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                                                                                                  Score 405.6; DB 8 Pred. No. 1.9e-86;
                                                                                                                            0; Mismatches
TE: 2003-03-17
NOS: 42514
                                                                                                    25.9%;
58.9%;
                                                                                                                              Conservative
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SEQ ID NO 25116
LENGTH: 2738
                                                                                                               Local Similarity
                                                              ; ORGANISM: HUMAN US-10-170-235-25116
                                                                                                  Query Match
Best Local Simi
Matches 767;
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Sequence 25116, Application US/10170235
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: TRANSCRIPTS, FOR DETECTING EXPRESSION AND OTHER USES THEREOF
FILE REFERENCE: CLO01380
CURRENT APPLICATION NUMBER: US/10/170, 235
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CTGTGCCTGGGATCCTTCGTGCCAGACGAGGTGAGGGGATCCAGGCCCCCAGTTTCTCCA
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                                    AGGACGCCCTATGTCAGGTGGAATTATGTGGCCCAAGAACTTTGCCCAGGCCCTGGGATGT
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; GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
; APPLICANT: GRUPE, Andrew
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US-60-452-680-8056
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: BEGOVICH, AM
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: RHEUMATOID ARTHRITIS, METHODS OF DETECTION AND USES THEREOF
FILER REPERENCE: CL001455, 444
CURRENT APPLICATION NUMBER: US/60/455, 444
CURRENT APPLICATION NUMBER: US/60/455, 444
CURRENT FILING DATE: 2003-03-18
NUMBER OF SEQ ID NOS: 50986
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2252
LENGTH: 2738
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Pred. No. 1.9e-86;
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58.9%;
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Matches 767; Conservative
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US-60-455-444-2252
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US-60-453-135-4736; Sequence 4736, Application US/60453135; GENERAL INFORMATION:
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TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1450
CURRENT APPLICATION NUMBER: US/60/452,680
CURRENT FILING DATE: 2003-03-07
NUMBER OF SEQ ID NOS: 116213
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8056
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                                                                                                                                                                    Score 405.6; DB 11; Length
Pred. No. 1.9e-86;
0; Mismatches 509; Indels
                                                                                                                                                                    Query Match . 25.9%;
Best Local Similarity 58.9%;
Matches 767; Conservative
                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
US-60-452-680-8056
                                                                                                       LENGTH: 2738
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APPLICANT: CARGILL, Michele
APPLICANT: CARGILL, Michele
APPLICANT: AKOUBOVA, Olga
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: WYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOM456
CURRENT APPLICATION NUMBER: US/60/453,135
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0 .. ښ 1401 1461 1696 TTACTCTGCTTTTATTCTCAAGAATGGTATGCACGTCAGCACTGTCCTCTGAAAAATCCC 1755 Gaps 1396 TCCAACTATTATAGAACCTGGAATGTGGTGCTCCATGACTGGCTATATTACTATGTATACTAC CAGGTCAGCCTGTACTGCCAGGAGTGGTACGCACGGCGGCACTGCCCCTTACCCCCAGGCA 287 CATCCCTGGGGAAACAGAAAGTTTTCATCATCGCAAGTCCCTGCTTGATGAGCTGATGG 1222 CAGGATGGGCTGCGGCTCCTTGGTGCCCGGGCCCGAGGGGTAGCCATGCTGGTGTTC 1456 AAGGACTITCTCCGAAGAGATTCAAATCTGCTGCCATTTAGCTGTTTT 1282 CTGGTCTCCGCAGTGGCCCATGAGTATATCTTCTGCTTCGTCCTGGGGTTCTTCTATCCC GTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACTTCATGATGCATGACCAG CGCACCGGCCGGCATGGAACGTGCTGATGTGCTGTTTCTAGGCCAGGGAATC AGGTGCAGCATTTCCGCACCATCTACCACATGTTCATCGCTGGCCTGTGTGTCTTCATCA TCAGCACCCTGGCCATCGACTTCATTGATGAGGGCAGGCTGCTGCTGGAGTTTGACCTAC CCACCCTGTTGGCGCCGTACCAGGCCCTACGGCTGTGGGCCCAGGGGCCACCTGGACGCAGG TCCAACTACTACCGCACTTGGAACGTGGTCCATGACTGGCTGTACAGCTACGTGTAT TGATCTTCAGCTTCGGACAGCTGCCATTGGCGCTGGTGACCTGGGTGCCCATGTTTCTGT 26; Indels 1522 ACTITICIGGGGGCTGGTGACACCTCGATCTTGGTCCTGCCAT 1563 DB 11; Score 405.6; DB 11; Pred. No. 1.9e-86; 0; Mismatches 509; 527 ò

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Pred. No. 1.9e-86;
); Mismatches 509;
Sequence 4736, Application US/60453050
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASS
TITLE OF INVENTION: STENOSIS, METHODS OF DET
TITLE REFERENCE: CL001457
CURRENT APPLICATION NUMBER: US/60/453,050
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEO ID NOS: 82762
SOFTWARE: FastSEQ for Windows Version 4.0
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58.9%;
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Best Local Similarity 58.9
Matches 767; Conservative
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US-60-453-050-4736
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LENGTH: 2738
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ID NOS: 42212

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NUMBER OF SEQ
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APPLICANT: Mullahy, Sara J.

APPLICANT: Mullahy, Sara J.

APPLICANT: Mullahy, Sara J.

APPLICANT: Mullahy, Sara J.

APPLICANT: Naudhcon, Rebecae B.

FILE REFERENCE: PD-1002 CIP

CURRENT RAPLICATION NUMBER: US/09/532,315B

CURRENT APPLICATION NUMBER: US/09/124

PRIOR FILING DATE: 1992-07-17

PRIOR FILING DATE: 1992-07-17

PRIOR FILING DATE: 1993-08-03

PRIOR FILING DATE: 1993-01-16

PRIOR APPLICATION NUMBER: 08/196.7

PRIOR PLICATION NUMBER: 08/196.7

PRIOR PLICATION NUMBER: US/008,119

PRIOR PLICATION NUMBER: US/01-14

PRIOR PLICATION NUMBER: US/198-01-16

PRIOR PLICATION NUMBER: PS/198-01-16

PRIOR PRIOR PLICATION NUMBER: PS/198-01-16

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PRIOR PLICATION NUMBER: PS/198-01-16

PRIOR PLING PAPELCATION NUMBER: PS/198-01-16

PRIOR PRIOR
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A RAPLICATION NUMBER: 08/438,571

PR FILING DATE: 1995-05-10

PR APPLICATION NUMBER: 08/179,873

PR FILING DATE: 1994-01-11

PR APPLICATION NUMBER: 08/504,732

PR FILING DATE: 1995-07-20
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FILING DATE: 1993-10-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGGGGTTCTTCTATCCCGTCATGCTGATACTCTTCCTTGTCATTGGAGGAATGTTGAACT 1384
                                                                                                                                                                                                                                                                                                                                                                                              965 TCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCGGTGCCCTGGTGCTCTTATCCTGC 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGCCACGTTGCCAGGCATCTTCATGCTGCTGCTCATCTTCTTTGCCTTCCATTGCT 1084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGCTCAACGCCTTTGCCGAGATGCTACGATTTGGAGACAGGATGTTCTACCGGGACTGGT 1144
                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCTTTGCCAACATGAGCCGAGAGCCCTTCAGCACCGGTGCCCTGGTGCTCTATCCTGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----GTGGCCCATGATATCTTCTGCTTCGTCC 362
                                                                                                                                                                                                                                                                                                             905 CCCAGGCCCTGGGATGTGTGCTCTATGCCTGCTTCATCCTGGGCCGCCTCTGTGTTTCCTG 964
                                                                                                                                                                                                                                                                                                                                                CCATGCTGGGTGTTCCTGGTCTCCGCAGTGGCCCCATGAGTATATCTTCTGCTTCGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 508;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                        Score 345.2; DB 6;
Pred. No. 2.8e-72;
); Mismatches 18;
                                                        NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: hu01263546
                                                                                                                                                                   or other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        completed: April 30, 2003, 15:28:10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTGTGCCACTGGAAGGGAGC 442
                                                                                                                                                                                                                        22.0%;
ilarity 84.8%;
Conservative
                                                                                                                                                                   ú
                                                                                                                                                                   ť,
                   ORGANISM: Homo sapiens
                                                                                                                                                             ; OTHER INFORMATION: a, US-09-532-315B-1168
                                                                                                                                                                                                                                                Similarity
                                                                                                                          NAME/KEY: unsure
                                                                                                                                             LOCATION: 497
                                                                                                                                                                                                                            Query Match
Best Local Simi
Matches 424;
TYPE: DNA
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(OTASU) AWAJB SDAY SIHI